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214605 i AC091618 Rattus norvegicu
228201 i AC016614 Mus musculus clo
271519 i AC020887 Mus musculus clo
878 i AC070284 Giardia intestinali
1241 i AF090137 Homo sapiens carbo
1458 i E16306 CDNA encoding kerata
2096 i X98341 B.subtilis orffMul DN
2190 i U65637 Homo sapiens chondro
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AFO66183 Porcine reproduct
AFO13266 Porcine reproduct
AF176348 Porcine reproduct
AF176348 Porcine reproduct
AF184212 Porcine reproduct
AF01575 Bacillus subtilis
AFO16565 Bacillus subtilis
AFO05665 Bacillus subtilis
AFO016665 Bacillus subtilis
AFO01666 Bacillus subtilis
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AFO01667 Bacillus subtilis
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AFO01618 Human chromosome
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258829 ACO73771 Mus musculus clo
166464 A.1158212 Homo sapiens chr
208632 ACO73711 Mus musculus clo
29 AXO05885 Sequence 94 from Pat
10064 1032811 Haemophilus influen
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AC074041 Mus musculus chr
AC074041 Mus musculus chr
AC075180 Homo sapiens clo
AL162400 Homo sapiens clo
AL027180 Homo sapiens clo
AC073658 Mus musculus clo
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AC091422 Mus musculus chr
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AF06834 Porcine reproducti
AF03356 Porcine reproduct
AF303355 Porcine reproduct
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S56481 beta 3-adrenergic re
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12 of 4) 16 of 8) 17 of 8) 18 of 4) 18 of 36 18	ALLO3194 Human Chromosome 14 1 AC008356 Drosophila melanoga 1 AL031658 Human DNA sequence
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Eukaryoth. Viriliplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Booldeae; Triticae; Triticae.

1 (bases 1 to 1872)
Peng,J., Richards,D.E., Hartley,N.M., Murphy,G.P., Devos,K.M., Filththam,J.E., Beales,J., Fish,L.J., Worland,A.J., Pellaca,F., Fellatham,A.J., Pellaca,F., Follaca,F., Sudhakar,D., Christou,P., Snape,J.W., Gale,M.D. and Harberd,N.P. (Green revolution' genes encode mutant gibberellin response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAE242531 1872 bp DNA PLN 28-JUL-1999
Triticum aestivum rht-Dla gene for gibberellin response modulator.
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Submitted (25-MAY-1999) Richards D.E., Molecular Genetics, John
Innes Centre, Colney Lane, NR4 7UJ, UNITED KINGDOM
Location/Qualifiers
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Harberd, N.P., Peng, J. and Richards, D.E.
Green revolution genes encode mutant glbberellin response
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  HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
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/organism="Triticum aestivum"
/db_xref="taxon:4565"
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gibberellin response modulator; rht-Dla gene.
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Ratio: 4.765
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldee; Triticae; Triticum.
1 (bases 1 to 453)
Harberd,N.P. and Peng,J.
Genetic control of plant growth and development
Patent: WO 9909174-A 66 25-FEB-1999;
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Sequence 105 from Patent WO9909174.
AX005896.1 GI:9928885
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Sequence 66 from Patent W09909174.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; (booldeae; Triticum. (bases 1 to 2709) Harberd, N.P. and Peng, J. (and Peng, J. (an
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Gaps: 0
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448
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452
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1444
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                                                                                   alignment_block:
US-09-485-529-104 x AX005805
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                                                                                                                                                                    to: AX005805
Ratio: 4.765
Percent Similarity: 100.000
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LOCUS AX005794
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                                                                                                                                                                                                                                                                                                                                                                                                                    ATAPADI.SADSVRDPKRMRTGGSSTSSSSSSSSSGGGARSSVVEAAPPVAAANATP
ALPVVVVDTOTGRGIRLVHALIACAEAVOGENISAAEALVKQIPLIAASQGGAMRKVAA
YFGEALARRVERFEPOPDSSI.LIDAAFADI.LIAHEYESCPYI.KAHFTANQAILEARAG
CRRVHVVDFGIKQGMQMPALLQALALRRGGPPSFRLIGVGPPQPDETDALQQVGWKLA
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EAERKVLGYRAVRPRLYVVEDEANNSGTFLORFTEELHYSGTWFDSLEGGSGGG
PSEVSGAAARPAAPLAGGTDQVMSEVYLGRQICAVVACEGAERTERHETLGQWRNELGNA
GFETVHLGSNAYRQASTLLALFAGGDGYRVEEKEGCLTLGWHTRPLIATSAWRLAGP"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 2125)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 14 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-AUG-2000
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/db_xref="GI:5640157"
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Gaps: 0
Percent Identity: 100.000
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/db_xref="taxon:4565"
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/db_xref="taxon:4565"
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Sequence 14 from Patent WO9909174.
                                                                                                                                                                 /gene="rht-Dla"
/note="GAI ortholog"
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US-09-485-529-104 x TAE242531
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Percent Similarity: 100.000
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BASE COUNT ORIGIN

us-09-485-529-104.p2n.rge

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1 (bases 1 to 302)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 16 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
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/note-"n is any nucleotide"
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LOCUS AX005807 302 bp DNA
DEFINITION Sequence 16 from Patent W09909174.
VERSION AX005807.1 GI:9928804
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US-09-485-529-104 x AX005794
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Ratio: 4.765
Percent Similarity: 100.000
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; 2ea.
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                                                                                                                                          I (bases 1 to 371)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 17 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
Gaps: 0 Caps: 0 Percent Identity: 94.118
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Gaps: 0
Percent Identity: 94.118
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Sequence 12 from Patent W09909174.
AX005803
AX005803.1 GI:9928800
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/db_xref="taxon:4577"
a 121 c 139 g
                                                                                                           Align seg 1/1 to: AX005807 from: 1
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US-09-485-529-104 x AX005807
 Quality: 78.00
Ratio: 4.588
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seq_documentation_block:
LOCUS AXV05806 2255 bp
AXV05806 Sequence 15 from Patent
ACCESSION AXV05806
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( (pases 1 to 1890)

Peng, J., Richards, D.E., Hartley, N.M., Murphy, G.P., Devos, K.M., Filntham, J.E., Beales, J., Fish, L.J., Worland, A.J., Pellca, F. Sudhakar, D., Christou, P., Snape, J.W., Gale, M.D. and Harberd, N.P., Green revolution' genes encode mutant gibberellin response
                  Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Enhartoidee; Oryzeae; Oryzea. Oryzea. Oryzea. Oryzeae; Oryzeae. O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZMA242530 1890 bp DNA PLN 28-JUL-1999
Zea mays partial d8 gene for gibberellin response modulator.
AJ242530
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/product="gibberellin response modulator"
/protein_id="CAB51557,1"
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Gaps: 0
Percent Identity: 94.118
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D8 gene; gibberellin response modulator.
Zea mays.
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/db_xref="taxon:4530"
252 c 294 g 120
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99347734

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    /organism="Zea mays"
    /db_xref="taxon:4577"

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LOCUS ZMA242530
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QASAAANGPAVPVVVDTQEAGIRLVHALLACAEAVQGENFSAAEALVKOIPMLASSO
GAMRKVAAPTEGALARVYRRPPPDSSLLDARABDLLHHFYESCYLKFAHFTAN
GAJLEAFAGCRRVHVDFGI KQGMQWPALLQALALREGGPPSFRLTGVGPPQDBETDA
LQQVGWKLAQFAHTIRVDFGI KQGMQWAATLADLEPFMLQPBGDDDDEPEVIAVNSVFE
EHRLAQAPGALEKVLGYPARPRIYVTVGQENHNSGTFLDRFTESLHIYYSTWEDSL
EGAGAGSGOSTDASPAAGGTDQWSEVYLGRQICNVYACEGARFTERHETLGQWRSR
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/translation="MKREYQDaGGSGGDWGSSKDKWMAAAAGAGEQEEEDVDELLAAL
GRYKNSSDBAADVAQKLEDLEMAAWGWGGAGATADDGFYSHLATDYHVRNSDISSW
VESMLSELNAPPAPLPAPAPRLASTSSTYSGAAGAGYFDLPAVDSSSSYYALK
PIPSPVAAPSADPSTDSAREPKRMRTGGGSTSSSSSSSSSSSSWDGGRTRSSVVEAAPPAT
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Patent: WO 9909174-A 15 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
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BARKVAAYEGBALARRYERAADSTLLDAAFBLLHAGESCPYLKEGERTERHETANGAI
LEAPAGCHRHYHVDEOTKOGNOMPALLOALLRPGGEPSFRLTGVGPPQPDETDALOV
VGWKLAQFAHTIRVDFQYRGLVAATLADLEPPHLQPEGEADANEEPEVTAVVSFELL
RLAQPGALEKVLGTYHAVRRYIVYVEQEANHINSGSFLDRFTESLHYYSTWEDSLEG
GSSGQABLSPPAGGGGGTDOVMSEVYLGROTCNVNACEGABRETERHETLGOMRINLG
RAGFEPVHLGSNAYKQASTLLALFAGGDGYRVEEKEGGLTLGHHTRLIATSAMRVA
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VESMLSELNAPLPP1PPAPPAARHASTSSTVTGGGGGGGFFELPAAADSSSSTYALRP1
SLPVVATADPSAADSARDTKRMRTGGGSTSSSSSSSSLGGGASRGSVVEAAPPATQG
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                                                                                                                                                                                                                                                                                                                                             Embryophyta; Tracheophyta;
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Sano, H., Ogawa, M. and Kusano, T.
Sano, H., Ogawa, M. and Kusano, T.
Direct Submission
Submitted (09-AUG-1999) to the DDBJ/EMBL/GenBank databases.
Mikhiro Ogawa, Nara Institute of Science and Technology, Plant
Molecular Breeding; Takayama 8916-5, Ikoma, Nara 630-0101, Japan
(E-mail: m-ogawa@bs.aist-nara.ac.jp, Tel:+81-743-72-5652,
                                                                                                                                                                                            30-MAR-2000
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                Oryza sativa (cultivar:Nipponbare) seedling cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                             Ogawa,M., Kusano,T., Katsumi,M. and Sano,H. Rice glbberellin-insensitive gene homolog, OsGAI, encode nuclear-localized protein capable of gene activation at
308 GATGAGCTGCTGGCCGCTCGGGTACAAGGTGCGTTCGTCGGATATGGC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 17
Gaps: 0
Percent Identity: 94.118
                                                                                                                                                                        AB030956 2500 bp mRNA PL
Oryza sativa mRNA for OsGAI, complete cds.
AB030956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .2500
/organism-"Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAA90749.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar-"Nipponbare"/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="GAI homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                771 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcriptional level
Gene 245 (1), 21-29 (2000)
20179680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="OsGAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="OsGAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="OsGAI"
                                                                                                                                                                                                                                                           AB030956.1 GI:6970471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax:+81-743-72-5659)
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Ratio: 4.588
Percent Similarity: 100.000
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US-09-485-529-104 x AB030956
                                                                                                                                                                    seq_documentation_block:
LOCUS AB030956
                                                                                                                          seq_name: gb_p1:AB030956
                                                                                                                                                                                                                                                                                                                           Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                (sites)
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                                                                                                                                                                                                                                                                                 OSGAI.
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                                                                                  358 G 358
                                        17 a 17
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DEFINITION
                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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                                                                                                                                                                                                                                                                                                   SOURCE
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Crowner dentified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genescan+ (Chris Burge, http://crowner.com/). And Genescan+ (Chris Burge, http://crowner.com/). Genescan+ (Chris Burge, http://crowner.com/). And Genescan+ (Chris Burge, http://genemark.biology.gatech.edu/Genemark/), and Genesplicer (Mihaela Perrea and Steven Salzberg, contact mpertea@tigr.org/, complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgl.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes without significant peptide similarity but with EST similarity to other proteins are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Simple repeats are predictified by repeatmasker (Arian Smit, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are http://tp.genome.washington.edu/RW/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Ehrhartoideae; Oryzae;
I (bases 1 to 122497)
Buell,C.R., Yuan,Q., Ouyang,S., Moffat,K.S., Hill,J.N.,
Gansberger,K., Brenner,M., Burgess,S., Hance,M., Shvartsbeyn,M.,
Tsitrin,T., Riggs,F., Hsiao,J., Zismann,V., Blunt,S., Pai,G.,
VanAken,S.E., Ufterback,T.R., Feldblyum,T.V., Quackenbush,J.,
Salzberg,S.L., White,O. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA (bases 1 to 122497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (25-JAN-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
3 (bases 1 to 122497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAC clone OSJNBb0022E02 is from Oryza sativa chromosome 3
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AC087797 122497 bp DNA PLN
DEFINITION Oryze sativa chromosome 3 BAC OSJNBb0022E02 genomic sequence,
complete sequence.
ACCESSION AC087797
VERSION AC087797.5 GI:13699786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (03-MAY-2001) The Institute for Genomic Research, 9
Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org
Medical Contest Dr. Rockville, MD 20850, USA, rbuell@tigr.org
Address all correspondence to:rice@tigr.org
(bases 1 to 122497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa.
                                                                                                                                                                                                                                                                                                                                   seq_name: gb_p1:AC087797
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DATRECYYLLKTROBALDYFI IT KAEVENOLDRY IK RERSDRGGEFFSNEFDLFCEF
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PNRKDKTPYPEINIGRKPSLSYLRTROCLAKTNAMLDTAGLPKAWWGEALLTSNHVLNRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAVRSEMDSIIANGTWEVTERPYGCKPVGCKWVFKKKIRPDASHGLLVHQMDVKTAFL
NGELDEEITYMDQPDGFVVEGQEGKVCKLLKSIYGLKQAPKOHHEKFDKTLITSAGFAVN
BADKCVYTRHGGEGVILLLXVDDILLIFGTNLEVINEVKSFLSGNFDMKDLGVADVIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MAAGSGARAVGDNGGGGVGGPPAPASLPLPPRHPSSPRRRTPA
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TEHTHELVSEEDVSEAPRRSKRQRTAKSFGDDFTVYLVDDTPKSISEAYASPDADYWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WMGAQARSGCEGNAESMAVALSACPYAGDLALAKGEATHGCGVMKGVIHGYVFITNSL
VCMYGKLGEMDNAKKAFRDATEKNIVTWNTLITSYATAGLCDEALDVLAQMEQIGGTV
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AQQTTNFKKQKKNNNNPNQDERTCFVCGQVGHLARKCPQRKGMKAPAGQTSKSANVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YPAVLEGYSDSNWISDVDEIKATSGYVFTLGGGAVSWRSCKQTILTRSTMEAELTALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATVEAEWLRDLLMDLPVVEKPTCEKT IEVCQEIKKLRSYNVGLHPNSEKPGRSLHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IITKCDRQCIEGDGFETHSILEGTHLCELDCWSQSMKILGESSRKLTKDLGV"
                                                                                   t="putative gag-pol polyprotein"
n_id="AAK50117.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21271. .21576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="GI:13937292"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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Percent Similarity: 100.000
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(5240. .1257)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSDNTENGEDDTNGAAFVFSITAPAQPNQTTGVATVREEL"

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EGTPPSAQYIPIFALFSPLFILQGAGVLFSLARLLEKVVLLLRNGPVSPNYLTISSKV
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EEVWRLQAALGEQSEITKCTKQEFERLQNEKVLCRICYEGEICMVLLPCRHRTLCKTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MRASVFTGVHSNVPLERVRQLGATLRPGCSSGGARNVGRGSTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein_id="AAK50133.1"
/db_xref="G1:13937302"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="predicted by glimmerR" 1386. .1640
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17887. .18048,18262. .>18366)
/gene="OSJNBb0022E02.12"
                                                                                                                                                                                                                                                                                                                                                        /note="predicted by fgenesh" complement(1271. .1579)
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/rpt_family="(GA)n"
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                                                                                                                                                                                                                                      complement(<1271, .>1579)
/gene="OSJNBb0022E02,11"
                                                                                                                                                                                                                                                                                              complement(1271. .1579)
/gene="OSJNBb0022E02.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <1386. .>1640
/gene="OSJNBb0022E02.18"
1386. .1640
/gene="OSJNBb0022E02.18"
                                                                                                                                                                                                                                                                                                                                                                                                             /gene-"OSJNBb0022E02.11"
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/gene="OSJNBb0022E02.18"
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                           /organism="Oryza sativa"
/cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
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                                                                                                                                                                                                        /clone="OSJNBb0022E02"
                                                                                                                                                /chromosome="3"
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Arabidossis thaliana Arabidossis thaliana Eukaryota; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots.
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I to 1951.
I to 1951.
Truong, H.N., Caboche, M. and Daniel-Vedele, F. Sequence and characterization of two Arabidopsis thaliana cDNAs isolated by functional complementation of a yeast gln3 gdh1 mutant FEBS Lett. 410 (2-3), 213-218 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (13-FEB-1997) H.N. Truong, INRA-Versailles, Laboratoire
de Biologie Cellulaire, Route de Saint-Cyr, 78026 Versailles Cedex,
FRANCE
                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Lichaes; Triticum.

1 (bases 1 to 324)
Harberd,N.P. and Peng,J.
Genetic control of plant growth and development Patent: WO 9909174-A 76 25-FEB-1999; HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="two-leaf stage seedlings"
/note="Landsberg erecta ecotype"
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Gaps: 0
Percent Identity: 100.000
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1. .1951
Acyaniam="Arabidopsis thaliana" /sub species="(L). Heynh" /db_xref="taxon:3702"
                                                                                                                                                                                                1. .324
/organism="Triticum aestivum"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                           'note-"n is any nucleotide"
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217
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141 c 85 g 56 t
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US-09-485-529-104 x AX005867/rev
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196. .1794
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Truong, H.N.
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                      Triticum aestivum
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Percent Similarity: 100.000
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LOCUS ATRGA2
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ISM Oryza sativa.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Eukaryota; Varidiplantae; Streptophyta; Euliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

ICE 1 (bases 1 to 725)
INS Harberd, N.P. and Pengy, J.
ISS Genetic control of plant growth and development Genetic control of plant growth and development Patent: WO 9909174-A 19 25-FEB-1999;

HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)

ES Location/Qualifiers
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                                                                                      6 others
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Gaps: 0
Percent Identity: 93.750
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226 c 276 g 119 t
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459
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/db_xref="taxon:4530"
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alignment_block:
US-09-485-529-104 x AC087797
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Ratio: 4.500
Percent Similarity: 100.000
                                                      Align seg 1/1 to: AC087797
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19-AUG-1997

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/db_xref="G1:233990"
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/db_xref="G1:233990"
/translation="MKRDHHHHQDKXTMMNNEEDDGNGMDELLAVLGYKVRSSEMAD VACKEQLEWMSNVQEDDLSQLATEPTHYNPARELYTWALDSATFDLKA IPGDAILNOPAIDSASSNOGGGGTOTTHRRLKCSNGVVETTTATABESTRHYVLVD SQENGVRLVHALLACAEAVQKENLTVAEALVKQIGFLAVSQIGAMROVATYFAEALRR
                                                                                                                                                                 RÎYRLSPSQSPIDHSLSDTLQMHFYETCPYLKFAHFTANQAILLEAFGGKKRVHVIDFS
MSGGLQWHALMALALRGGPPYELTGGPPAPBUBYLHEFWGCKLAHLAEA.HWEF
EYRGFVANTLADLLDSAHLELRSEIESVEWNSYFELHKLIGREGAIDRVLGWQIKP
EIFTVVEQESNHNSPIFLDRFTESLHYYSTLFDSLEGVPSGODKVMSSEVYLGKOICNW
                                                                                                                                                                                                                                             VACDGPDRVERHETLSQWRNRFGSAGFAAAHIGSNAFKQASMLLALENGGEGYRVEES
DGCLMLGWHTRPLIATSAWKLSTN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENKARYOTE; VITIGIPLANTAE; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosladae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1964)
Harberd, N.P., Peng, J., Carol, P. and Richards, D.E.
NUCLEIC ACID ENCODING GAI GENE OF ARABIDOPSIS THALIANA
PATENTE: MORTE INNOV LID (GB)
INNES JOHN CENTRE INNOV LID (GB)
Other publication AU 1799697 19970828.
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Gaps: 0
Percent Identity: 82.353
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Gaps: 0
Percent Identity: 82.353
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/strain="LANDSBERG ERECTA"
/db_xref="taxon:3702"
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Sequence 1 from Patent W09729123.
A64697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: ATRGA2 from: 1 to: 1951
/codon_start=1
/product="RGA2 protein"
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/haplotype="GAI"
426 c 474
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Ratio: 4.118
Percent Similarity: 100.000
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Percent Similarity: 100.000
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SOURCE
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Large Class.

Surface Class.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatorphyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

El (bases 1 to 1964)

Speng,J., Carol,P., Richards,D.E., King,K.E., Cowling,R.J., Murphy,G.P. and Harberd,N.P.

The Arabidopsis GAI gene defines a signalling pathway that negatively regulates gibberellin responses

Al Genes Dev. In press

El 2 (bases 1 to 1964)

Sharberd,N.P.

Blirect Submission

Al Couley Lane, Norwich, NR4 7UJ, UK

Conetics, Colney Lane, Norwich, NR4 7UJ, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTEMBL:023724"
/translation="MKRDHHHHQDKKTMMNBEDDGNGMDELLAVLGYKVRSSEMAD
/translation="MKRDHHHHQDKKTMMNBEDDGNGMDELLAVLGYKVRSSEMAD
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SQENGYRLYHALLAGARAVQKBHLYMRALYKQIGFLAVSQLGAMRKYATYFRALAR
RIYRLSPSQSPIDHSLSDTLQMHFYETCPYLKFAHFTANQAILEAFQGKKRVHUDFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSQGLOWPÄLMQALALRPGGPPVFRLTGIGPPAPDNFDYLHEVGCKLÄHLAEAIHVEF
SKGFVANTLALDLASMLELRPSEIESVANVSYFELHKLLIGRPGAIDKYLGVVNOIKP
EIFTVVEGESHHNSPIFLDRFFESLHYYSTLEDSLEOVPSGORVWSEYVLGGOICNV
VACDGPDRVERHETLSQWRNRFGSAGFAAHIGSNAFKQASMLLALFNGGEGYRVEES
                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
                                                                                                             PLN
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Percent Identity: 82.353
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/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/chromosome="1"
209. .1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/protein_id="CAA75492.1"
/db_xref="GI:2569938"
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                                                                   to: 1964
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                                                                   from: 1
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209. "
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/gene="GAI"
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Arabidopsis thaliana
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Y15193.1 GI:2569937
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US-09-485-529-104 x ATY15193
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Percent Similarity: 100.000
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alignment_block:
US-09-485-529-104 x A64697
                                                                 Align seg 1/1 to: A64697
                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS ATY15193
                                                                                                                                                                                                                                                                                                       seq_name: gb_pl:ATY15193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAI gene.
thale cress.
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273 GATGAGCTTCTCGCTGTTTTAGGTTACAAAGTTAGGTCATCGGAGATGGC 322
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Percent Similarity: 100.000
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US-09-485-529-104 x ATRGA1
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LOCUS ATRGA1
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                                                                                                                                          seq_name: gb_pl:ATRGAl
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                                                                                                  323 G 323
                                                            a 17
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ORIGIN
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VRLVHALMACAEAIQONNLTLAEALVKOIGCLAVSQAGAMRKVATYFAEALARRIYRL
SPPONDIDHOLLSDTLOMHYTETCPYLKFAHFTANQAILEAFECKRYRIYIDFSMNGGL
GWPALMOALALREGGPPTRITGIGPPAPDNSDHLHEVGCKLAOLAEAVHYEFEYRGF
VANSLADLDASMLELRESDTEAVAUVYFELHKLLGERGGIERVLGVVKQIKPVIFTV
VEQESNHNGPVFLDRFTESLHYYSTLFDSLEGYPVSQPKYGIKPVIFTY
VEQESNHNGPVFLDRFTESLHYYSTLFDSLEGYPVSQDKYWSEYYLGKQICNIVACEG
PDRVERHETLSQWGNRFGSSGLAPAHLGSNAFKQASMLLSVFNSGOGYRVEESNGCLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MKRDHHQFQGRLSNHGTSSSSSISKDKMMVKKEEDGGGNMDD
ELLAVLGYKVRSSEMAEVALKLEQLETMMSNVQEDGLSHLAADTVHYNPSELYSWLDN
MLSELNPPPLPASSNGLDPVLPSPEICGFPASDYDLEVIPGNAIYQFPAIDSSSSSNN
                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Epematophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae: eurosids II: Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 2201)
Peng, J., Carol, P., Richards, D.E., King, K.E., Cowling, R.J.,
Murphy, G.P. and Harberd, N.P.
The Arabidopsis GAI gene defines a signalling pathway that
negatively regulates gibberellin responses

2 (bases 1 to 2201)
Harberd, N.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (22-OCT-1997) N.P. Harberd, John Innes Centre, Molecular
Genetics, Colney Lane, Norwich, NR4 7UJ, UK
Location/Qualiflers
                                                                                                                                                                                                                                                                                    01-NOV-1997
                                                          1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                    PLN
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Gaps: 0
Percent Identity: 82.353
                                                                                                                                                                                                                                                                                  ATY15194 2201 bp mRNA ATADIdopsis thaliana mRNA for GRS protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="GRS protein"
/protein_id="CAA75493.1"
/db_xref="GI:2569940"
/db_xref="SPTREMBL:023725"
                       to: 1964
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                    to: ATY15193 from: 1
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/codon_start=1
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Percent Similarity: 100.000
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LOCUS ATY15194
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                                                                                                                                                                                                                        seq_name: gb_pl:ATY15194
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                    Align seg 1/1
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ACCESSION
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KEYWORDS
SOURCE
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MLSELNPPPLPASSNGLDPVLPSPEICGFPASDYDLKVIPGNAIYQFPAIDSSSSSNN
ONKRIKGSSSSSPSSMYTSGYSTGYDIGGYTGTTYTTTTTAAABSTRSYILVDSGDENG
VNKRIKAGSSSSPSSMYTSGYSTGYDIGGYTGTTYTTTTTTAAABSTRSYILVDSGDENG
VNKRIMAACABAIQONNLTIABAIVKQIGCLAVSQAGAMRVVATYRABALABITRSIYL
SPPQNOIDHCLSDTLQMHFYETCPYLKFAHFTANQAILBAFEGKKRVHVIDFSMNGGL
VMPALMQALALREGGPPTFRLTGIGPPADNSDHILBVGGKAKAQLABAITVEREYRGF
VMNSLADLDASMLERPSDTBANAVNSVFELHKLLGRPGGIEKVLGVVKQIKPYIFTV
VEQESHHNGPVFLLARFGSLHYYSTLFDSLEGVPNSQDKVMSEVYLGKOICNLVACEG
                                                                                                                                                                                                                                                                                                                                                                                                     Truong, H.N.
Direct Submission
Submitted (13-FEB-1997) H.N. Truong, INRA-Versailles, Laboratoire
de Biologie Cellulaire, Route de Saint-Cyr, 78026 Versailles Cedex,
FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKRDHHQFQGRLSNHGTSSSSSSISKDKWMVKKEEDGGGNMDD
ELLAVLGYKVRSSEMAEVALKLEQLETMMSNVQEDGLSHLATDTVHYNPSELYSWLDN
                                                                                                                                                                                                                      1 (bases 1 to 2210)
Truong, H.N., Caboche, M. and Daniel-Vedele, F. Sequence and characterization of two Arabidopsis thaliana cDNAs isolated by functional complementation of a yeast gln3 gdh1 mutant FEBS Lett. 410 (2-3), 213-218 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDRVERHETLSQWGNRFGSSGLAPAHLGSNAFKQASMLLSVFNSGQGYRVEESNGCLM
                                                                                                                                                                                            Tracheophyta;
19-AUG-1997
                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheof
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="two-leaf stage seedlings"
  PLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .2210 /organism="Arabidopsis thaliana" /sub_species="(L). Heynh" /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note-"Landsberg erecta ecotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAA72177.1"
/db_xref="GI:2339978"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="RGA1 protein"
                   A.thaliana mRNA for RGAl gene.
Y11336.1 GI:2339977
RGAL gene.
thale cress.
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132. 1895
/gene="RGA1"
  2210 bp
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Light Class: thaliana plantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatorphyta; magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Esto,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E., Kotani,H., Tabata,S., Mewes,H.W., Rudd,S., Lemcke,K. and Mayer,K.F.X.

L Unpublished

E (bases 1 to 24604)

E (bases 2 to 24604)

E (bases 3 to 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATK3M16 26604 bp DNA PLN 07-AUG-2000
Arabidopsis thaliana DNA chromosome 5, BAC clone K3M16 (ESSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1968 GACGAGCTTTTGGTTGTTTAGGTTACAAAGTTCGATCATCCGACATGGC 2017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                    Length: 17
Gaps: 0
Percent Identity: 82.353
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/db_xref="taxon:3702"
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90. 224
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/gene="K3M16_10"
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90. .3656
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1530, .1880
/gene="SCR2"
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  1434. .1529
/gene="SCR2"
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1881. .3410
/gene="SCR2"
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Quality: 70.00
Ratio: 4.118
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/translation="MEEVSEMEVEVONROLSDSSPAQNVKKFGLKNSIQTNFGSDYV
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LSDETVHYNRSDLGSWVESMLSDLDPTRIQEKPDSFFDLARAFGSAVYPRDEHYTRS
KRTEIESELSSTRSVVLDSQETGVRLVHALLACAEAVQNNLKLADALVKHVGLLAS
SQAGAMRKVATYFRAGLARRIYRIYRDDVASSSFSDTLQIHFYESCPYLKFAHFTAN
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GWKLGQLASTIGVNFEFKSIALNNUSDLKFPENLDIRPGLESVAVNSVFELHHILAHPG
SIDKFLSTIKSIRPDIMYTVEQEANHNGTVFLDRFFESLHYYSSLFDSLEGPPSQDRV
MSELFLGRQILNLVACEGEDRYBERHETLNOWRNRFGLGGFRVVSIGSNAYKQASMLLA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

( (Asses 1 to 4081)
Sanchez-Fernandez, R., Ardiles-Diaz, W., Van Montagu, M., Inze, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-MAR-1998) Sanchez-Fernandez R., Department of Genetics, University of Gent (VIB), K.L. Ledeganckstraat 35, 9000
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join(900. 1048,1130. 1343,1434. 1529,1881. 3410)
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1434. 1529,1530. 1880,1881. 3410)
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/gene="SCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning of the Arabidopsis thaliana RGA-like gene, a putative member of the VHIID domain transcription factor family Unpublished
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LYAGADGYNVEENEGCLLLGWQTRPLIATSAWRINRVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA12242.1"
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1130. .1343
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/number=2
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/gene="SCR2"
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Sanchez-Fernandez, R.
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3560. 3637 /gene="K3M16_10" /number=11 3638. 3656 /gene="K3M16_10" /number=12 5627. 5704 /gene="K3M16_20"		APGMYDKRAPAGHIRNPTQSFPTANAPEENYVSLFSDDNVHAACSIM" 57056046 /gene="K3M16_20" /number=1 60476122 /gene="K3M16_20"	્રા ભ	78239866 /gene="K3M16_30" complement(join(78238600,86908795,89268974, 90629142,96819866)) /gene="K3M16_30" complement(join(78238600,86908795,89268974,	9062. 9142. 9681. 9866)) /gene="K3M16_30" /codon_start=1 /product="hypothetical protein" /protein_id="CACO1890.1" /db_xref="GACO1890.1" /db_xref="GACO1890.1" /db_xref="GACO1890.1" /translation="MYPPACYOCGTRONPCRCKVVGPTLGFVAFLITGIIEWPVGAVV /translation="MYPPACYOCGTRONPCRCKVVGPTLGFVAFLITGIIEWPVGAVV /translation="MYPPACYOCGTRONPCRCKVVGPTLGFVAFLITGIIEWPVGAVV /translation="MYPPACYOCGTRONPCRCKVVGPTLGFVAFLITGIIEWPVGAVV /translation="MYPPACYOCGTRONPCRCKVVGPTLGFVAFVAFLY /translation="MYPPACYOCGTRONPCRCKVVGFTLGFTGFTFTAFVAFTLATION-" /translation="MYPPACYOCGTRONPCRCKVVGFTLGFTGFTFTAFVAFTLATION-" /translation="MYPPACYOCGTRONPCRCKVGFTTAFVAFTLATION-" /translation="MYPPACYOCGTRONPCRCKVGFTTAFVAFTTAFVAFTLATION-" /translation="MYPPACYOCGTRONPCRCKVGFTTAFVAFTLATION-" /translation="MYPPACYOCGTRONPCRCKVGFTTAFVAFTLATION-" /translation="MYPPACYOCGTRONPCRCKVGFTTAFVAFTLATION-" /translation="MYP	LINAANR COMPLEMENT(78238600) /gene="K3M16_30" /number=1 COMPLEMENT(86018689) /number=1 COMPLEMENT(86908795)	/ number=2 / number=2 / number=3 complement(89268974) /gene="K3M16_30" / number=3 complement(89759061) / gene="K3M16_30" / number=4 / number=4
intron exon exon gene CDS		intron	intronexon	gene gene CDS		exon intron exon	intron exon intron exon
/note="similarity to cisplatin resistance-associated overexpressed protein - Homo sapiens, EMBL:AB034205" /codon_start=1 /product="putative protein" /product="putative protein" /protein_id="CaC0188.1" /db_xref="G1:9755768".1" /db_xref="G1:975768".1" /db_xref="G1:97578".1" /db_x	/number=1 706. 858 /gene="K3M16_10" /number=2 859953 /gene="K3M16_10"	9541017 /gene="K3M16_10" /humber=3 /gene="K3M16_10" /gene="K3M16_10" /humber=3	12701349 /gene="KaM16_10" /number=4 13501431 /gene="KaM16_10" /number=4	/gene="K3M16_10" /humber=5 1580. 1935 /gene="K3M16_10" /number=5 1936. 1997	/gene="K3M16_10" /number=6 1998. 2236 /gene="K3M16_10" /number=6 2237. 2299 /gene="K3M16_10" /number=7 /gene="K3M16_10" /number=7 /gene="K3M16_10" /gene="K3M16_10" /gene="K3M16_10" /gene="K3M16_10" /gene="K3M16_10"	/ number e 27343036 /gene="K3M16_10" /number=8 30373118 /gene="K3M16_10" /number=9 3103 22.03	/gene="k3M16_10" /umber=9 320
intron	exon intron	exon intron	exon intron exon	intron exon	intron exon intron exon	intron	exon intron exon

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Counce were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur repm.orn.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/netpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html).

Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, that are predicted by sinilarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are predicted by tRNAscan-SE (Sean Eddy, the seas encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://ftp.genome.wasth.acu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, thtp://ftp.genome.wasthington.edu/RW/RepeatMasker.html). Regions of genomic sequence that are nonctated as genes but have predicted exons by GRAIL are annotated as misc features.
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4240. .4344,4437. .4547,4629. .4670,4860. .4973,5097: .5254,
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join(3627. .3661,3762. .3843,3918. .3995,4081. .4140,
4240. .4344,4437. .4547,4629. .4670,4860. .4973,5097. .5254,
5361. .5494,5576. .5682,5785. .5827,5903. .6144)
/gene="IIIP5.2"
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1459. .1593,1682. .1748,1837. .2055,2146. .2340,2492. .2879,
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SKFTIPQDITMLESF"
orientation of the sequence is from SP6 to T7 end of the BAC
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    .24217
    /note="overlap with BAC clone T12J13 (AC009327:65718. .89934)."

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/organism="Arabidopsis thaliana"
/orlitvar="Columbia"
/db_xref="taxon:3702"
/chromosome="III"
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/gene="T21P5.1"
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/gene="T21P5.1"
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Lin, X., Kaul, S., Town, C.D., Benito, M., Creasy, T.H., Haas, B., Ronning, C.M., Koo, H., Fujil, C.Y., Utterback, T.R., Barnstead, M.E., Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M.
Arabidopsis thaliana chromosome III BAC T21P5 genomic sequence
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Rockville, MD 20850, USA
e-mail: xlinftigr.org
BAC clone T21P5 is from Arabidopsis chromosome III and is near the molecular marker mi172.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-JAN-2001) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Jan 24, 2001 this sequence version replaced gi:12280866. Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                       /gene="K3M16_40"
complement(11207. .11647)
/gene="K3M16_40"
/note="strong similarity to calmodulin-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:

LOCUS ATAC009895 82289 bp DNA PLN 24-JAN-2001
DEFINITION ARADIdopsis thaliana chromosome III BAC T21P5 genomic sequence,
complete sequence.

ACCESSION AC009895
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Gaps: 0
Percent Identity: 82.353
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The Institute for Genomic Research
                                                                                                                                                                                complement(11207. .11647)
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complement(9143. .9680)
                                                                              .9866)
                                                                      complement(9681.
/gene="K3M16_30"
                                                                                                                                                                                                                                                                                                                                         /gene="K3M16_40"
11207. .11647
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US-09-485-529-104 x ATK3M16/rev
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Ratio: 4.118
Percent Similarity: 100.000
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                                                                                                                                                    /number=5
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complement(14488. .14563)
/note="exon predicted by xgrail, quality
excellent_shadowexon"
14893. .14935
/note="exon predicted by xgrail, quality marginal"
join(<15141. .15586,15675. .15872,16258. .16667,16780. .16950,17036. .>17427)
/translation="MAFFKGSESYPIKTIVVLVQENRSFDHTLGWFKELNREIDGVM
KSDQKRNPGFSSDLNSHNVPFGDQSQYVDPNPGHSIRDIYEOVFGKPMDSGHPDPNPG
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RLFIHSATSHGTTNNEKLLIEGFPOKTIFESLDEAGFTFGIYYQCFPTTEFRNLKK
LKYLTRFHDYGLOFKKDCKEGNLPNYVVEQRWYDLLLNPANDDHPSHDVSEGQKLVK
BYYBALKSSPQNNEILFITYDEHGGFYDHVPTDGVPNPDOTLGPPRYNFRENLG
RYVPTFFISPSPQNPETLSNPVKMRGYYBKSDLDGYPNDFDLGJAPNSGAPTRENRLG
FESVITRNSPRQDCFETLSNPVKMRGTYAKENRELSDFQVKTFKLKDFLTKRDSWAGT
FESVITRNSPRQDCFETLSNPVKMRGTYAKENRELSDFQCEELVIVAAGLKGDYKNEEL
LYKLCKKTCSDASKYVTKAFDKFVEESKKARERGGDENDIVFCVDDDDDHNVVKPPP
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brasslcaceae; Arabidopsis.

1 (bases 1 to 85702)
Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B.J.,
Wu,D., Maitl,R., Ronning,C.M., Koo,H., Fujil,C.Y., Utterback,T.R.,
Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thallana chromosome 1 BAC T27F4 genomic sequence
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The orientation of the sequence is from SP6 to T7 end of the BAC
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BAC T27F4 genomic sequence,
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Town,C.D. and Kaul,S.
Direct Submission
Submitted (19-3AN-2001) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdtcwn@tigr.org on Jan 19, 2001 this sequence version replaced g1:12280876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38963 GATGAGCTTCTTGCTGTTCTTGGCTACAAGGTTCGATCTTCTGAGATGGC 39012
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Gaps: 0
Percent Identity: 82.353
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LOCUS AC020665 85702 bp DNA
DEFINITION Arabidopsis thaliana chromosome 1
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AC020665.6 GI:12324388
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Lin, X. and Kaul, S.
Direct Submission
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US-09-485-529-104 x ATAC009895
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Ratio: 4.118
Percent Similarity: 100.000
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.13085,13162. .13332,
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LIDBEDDSSSSSDFSPLLIALIGILASAFILVSYYTLISKYCHRRHNSSSTSAAINRI
SSDYTWQGTNNNNNGATNNNNGATNPNQTIGGGGDGLDEDSLIKSITVYKYRKMDGFVESSDCS
VCLSEPQBNESLRLLEPKCHRATPCIDTWLKSHSNCPLCRAFIVTSSAVETVDLTNO
QIVTENNSISTGDDSVVVVULDLENSRSRNETVNEGSTPTXGDAGFKRRRAEIGVVK
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                                                                                                                                                                                                                                                                                                                                           quality
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13418. ,13761)
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complement(7082, .7166)

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complement(7109, .7231)

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complement(7036. .7205)
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                                                                                                           complement(7038. .7208)
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus."
                 DNA transposon - a consensus."
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                                                complement(6991. .7205)
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(Plant Mol. Biol. 34 (1), 57-68 (1997))"
complement(join(1757. 1964, 2044. 2152,2244. 2346,
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3625. 3702,3870. 3945,4033. 4088,4206. 4275,4478. 4642))
                                                                                                                                                                                                                                                                                                                                                                  Similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/Repeatmasker.html).
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FEPHDLKDSNDAPTVSRVLDFMLGWHLEPTTSGDYPQIMKDLLGYRLPQFTAAQKAKL
KDSTDFVGLNYYTSTFSNYNEKPDPSKPSWKQDSLVSWEPKNVDHSAIGSMPLTAALP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPQDLEDEYGGFLSQNIVKDFREYADYVFTEYGGKVKNWITFNEPWVFAHAGYDLGKK
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FLAQGVRPSALKRDEL"
Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR.081.mit.edu/GENSCAN.html), GeneMarkHwM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMarkh), GlimmerA (a variant http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea, du/GeneMark/), GlimmerA (a variant http://www.tigr.org/softlab/glimmerm_html/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tb/tgi.shtml), Annotated genes are named to indicate the level of evidence for their annotation, Genes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKNLNTDAFRLSIAWSRIFPHGRKEKGVSQAGVQFYHELIDELLKNGIVPFVTVFHWD
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 SIMPLEGUY1 is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="SIMPLEGUY1|SIMPLEGUY1 SIMPLEGUY1 is a
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 SIMPLEGUY1 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="beta-glucosidase, putative; 4642-1757"
/protein_id="AAG52157.1"
/db_xref="GI:12324390"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"/cultivar="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="T27F4"
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.orn.igov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGenes/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy/tRNAscan-SE). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats were numbered from the top to bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabate for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAFDYSLEMCIHLKKSAYLALIGNFLRSNELPKVIEVVKEMVKAQHSLGCYQGAMLIH
RLGFGRRPRLAADVFDLLPDDQKGVAAYTALMDVYISAGSPEKAMKILREMREREIMP
SLGTYDVLLSGLEKTSDFQKEVALLRKEKKSLVASARFRENVHVEDKICDLLFATNLL
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                         The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This work was supported by the National Science Foundation,
Department of Energy and the US Department of Agriculture.
On Dec 17, 1999 this sequence version replaced g1:3785968.
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/gene="At2g01390"
/note="F219.1; predicted by genscan"
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/note="F219.2; predicted by genscan"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at@tigr.org
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301. .>95137
hote="Sequence from clone F219"
<341. .>997
/gene="At2g01390"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="II"
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join(<1175. .1294,1620. .>1940)
/gene="At2g01400"
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                                                                                                                       (http://www.tigr.org/tdb/at/at.html).
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Location/Qualifiers
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   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(<14953. .15216,15304. .15444,15534. .>16490))
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AC005560.2 GI:6598472
                                                                                /product="beta-glucosidase, putative; 11384-8406"
/product="beta-glucosidase, putative; 11384-8406"
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TPODLEDBYGGFLSRNIYKDFREXADYVFTSTGGKVKNWITPUREPWYFAMD
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TPODLEDBYGGFLSRNIYKDFREXADYVFTSTGGKVKNWITPUREPWYFAMDHAFANGKYKGGKIGIAHSPAW
                                                                                                                                                                                                                                                                                                                                        FEPHDLKDSNDVPTVSRVLDFMLGWHLDPTTFGDYPQIMKDLLGHRLPKFTSSQKAKL
KDSTDFVGLNYYTSTFSNHNEKPDPSTPSWRQDSLVAWEPKNVDHSAIGSQPLTAALP
VYAKGFRSLLKYIKDKYANPEIMIMENGYGDKLKDKDSVEVGTADYNRKYYLQRHLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                      MNEAICIDKVRVTGYFVWSLLDNFEWQDGYNNRFGLYYVDFKNNLTRYEKESAKYYKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="contains Pfam profile: PF00646 F-box domain'
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Gaps: 0
Percent Identity: 82.353
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complement(14953. .16490)
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11220. .11384))
/gene="T27F4.3"
                                                             /codon_start=1
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Ratio: 4.118
Percent Similarity: 100.000
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US-09-485-529-104 x AC020665
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LOCUS AC005560
DEFINITION Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_pl:AC005560
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AUTHORS
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AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 132699)
Chao, C., Shinn, P., Dunn, P., Buehler, E., Kahn, S., Kim, C., Walker, M., Williams, S., Altafi, H., Araujo, R., Conn, L., Conway, A.B., Gonzalez, A., Hansen, N.F., Hutzar, L., Kremenetskala, I., Lenz, C., Li, J., Liu, S., Luros, S., Rowley, D., Schwartz, J., Toriumi, M., Vysotskala, V., Yu, G., Davis, R.W., Federspiel, N.A., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MecDnvDDFIDKKSDEQVKRDLVLACKRFPSIILGDSRPVELYS
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SLRAPEDLSHNAEDKAGKSIFLHLKKFPRGTRFTWQPPFLNSIDSHPGLSGLVISSKVK
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PANNDPIFELNKFRGTNFTHAVAGGRPYPITYPSKGLNNFFLSDVISRALRV
PANNDPIFERREYNIDVLADEESSHRAGGRPYPITYPSKGLNNFFLSDVISRALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLQSLGTKIEKDVLLEKFRKPVLNSVYIEEWSTLTKSFLKALPYSLTPSQLSAVSEII
WDLKRPVPMNRLLQGDVGCGKTVVAFLACMEVIGSGYQAAFMAPTELLAIQHYEQCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLENMEGDLQSGAISFIIGTHSLIAEKIEYSALRIAVVDEQORFGVIQRGKFNSKLYG
TSMISKSGSSDSDDTSKADLSMAPHVLAMSATPIPRSLALALYGDISLTQITGMPLGR
IPVETHIFEGNETGIKEVYSMMLEDLKSGGRVYVVYPVIDQSEQLPQLRAASAELEIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana BAC F10B6 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ecker, J.R.
Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-FEB-1999) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
                                                                                                   complement(join(20954. .21559,21680. .21763,21869. .2202
22234. .22377,22526. .22606,22742. .22813,23017. .23250,
23352. .22441,22559. .23640,23906. .24069,24308. .24542,
24746. .24858.24942. .25415))
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/db_xref="GI:3785974"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 17
Gaps: 0
Percent Identity: 82.353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to reverse of: AC005560 from: 1
    complement(<20954. ,>25415)
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/note="F2I9.6"
                                                                                                                                                                                                                                                                                                                           /codon_start=]
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Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-485-529-104 x AC005560/rev
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Genomic sequence for
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Percent Similarity: 100.000
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LOCUS AC006917 1
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TITLE
JOURNAL
            gene
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KEYWORDS
SOURCE
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complement(join(<14558. .14916,16258. .16337,16458. .>16607))
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/gene="At2g01430"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(<20954, .21559,21680, .21763,21869, .22027, 22234, .22377,22526, .22606,22742, .22813,23017, .23250, 23352, .234441,233559, .23640,22906, .24069,24308, .24542, /gene="At2g01440"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(14658. .14916,16258. .16337,16458. .16607))
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/tb_g1f="G1:3785971
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complement(join(6967. 7404,7509. 7585,7680. 7837,
8215. 8300,8400. 8707,8865. >10059))
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PRPSMLFARGEIYSLSSTPRGSNFWADFYSTSPAPNPERSTGTGVSTRDWKIPKENQOQ
OEKDSKASHDAKELHMFVWSSSASPVSDVFGGGGAGDNVATEQSEGGAKEIRWVVSDQP
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rlhreveelramkvgpttvnsassllymcprcervtpaaspsravvpvpakktfppqer
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PSTVWTRILILIMVWRKLISTNPWTYSZELIGLIMALAYRWHVAMPKILGGSISILSDAG
IGMANFSLGIEMALOPKIIAGSNSVATFAMAVRFITGPAIMAVAGIATGLHGDLIRIA
IVQAALPQGIVPFVFAKEYNVHPTILSTGVIFGMLIALPITLVYYILLGI.
                                                                                                                                                                                                                                    /translation="MARSCSIWTPVLISLSPVTGESPKISRRRVILATSIGSPQPLLE
AKIKEPQKLQVLDSKDVSRRNTMLYLAAGFLGGINFLNGEAAEARVGRKENRKKALEK
LRAKAKESEPNNKSGNQKIEKELEKEEVFPLLPPPLVVEANLLQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVDFKGNAYVTNSAKNFIWKVDRDGAASIFSKSPLFNSQPVAADADASFRDCGLNGIV
YISKGYLLVVQSNTGKVFKVDEDSGNARLVLLNGDLIAADGMTRRRRDGTVMVVSQKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement join (7338. 7404,7509. 7585,7680. 7837,8215. 8300,8440. 8707,8865. 10059))
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/db_xref="GI:3785973"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"putative auxin transport protein"
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/gene="At2g01410"
/note="F2193.3; predicted by genefinder"
complement(2069. .3232)
/gene="At2g01410"
join(1175. .1294,1620. .1940)
/gene="At2g01400"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="At2g01420"
/note="port
                                                                                                                                                                                                                                                                                                                                                                complement(<2069. .>3232)
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/db_xref="GI:3785970"
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COMMENT

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GIAGKNSKAEFQAPCRTTKYPREIPPLPWYRSAIPQWAWAGFLPFSAIYIELYYIFAS
VWGHRIYTIYSILFIVFIILIIVTAFITVALTYFQLAAEDHQWWWRSFLCGGSTGLFI
YAYCLYYYYARSDWSGFWQTSFFFGYMACICYGFFLMLGTVGFRAALLFVRHIYRSIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFDLSSFGEGNSRIMSKSGGFNLFVRAYFAFLDRRSILFHDGNRHRYNEESSVLIRLY
IIRKMQIIVDSLIRIKPIGENMAIPVINEAMENVVSEIMEIYGWICRRIAEVLPNVHS
KIGKTEADLALKIVAKSMKQGGELKKYFEFCKDLGVSNAQEIPNFVRIPEADVIHLDE
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YPEEVELSCLGESREALCSPREGSKYTRGQALKVGTSLTFVGFBARRDKAGNLMTQKSK
EQSLIVFSBESSFDBWYNNNKSQSELCVILAKIFGSIAVAIAVVYGVDYARKVLLPFV
WKKRDLGDSSSQNGSDSEDPDISDF"
                                                                                                                                                                                                                                                                                                                                          /translation="MDLSREVDDFIKETIDHSLGLPISMDVLQKKLYTAEESQRRLRE
QYLSLVSRLKEKEKVIDLVRSEASMNAQSLKKFVBENQKLGSEREDLVNQCKKWEKEC
FLYHQDRESLMEFGNETDERAREAESRVRELEEEVRKMSDEIKSRIESFEDCLVDSIL
                                                                                                                                                                                                                                                                                                                                                                                                                             ASFVSKDESISLGRIFLEANSEDKCCETLLRKWDOLKPTTOKFVSLVSWYRREKEK
ECLIMNLAKAEQEVELVSEQNRELDRENRKFLRQCSAERSHGSNKFNKRKSIKMMSSP
IEKRIELSSQEFID"
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DLISF"
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RSYHRRIDVISSPQINHTRFPFTSLRRVKQLARLKWKTAEERNEEEEDDTEETSTEEK
MTVQRRRKSKFTAEQREAMKDYAAKLGWTLKDKRALREEIRVFCEGIGVTRYHFKTWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKLWKRAAVVLKDGPSLIAADDILTAAVVKATSHDELSIDTESA
QFIYRHVLSSPSSLKPLVSLISSRVKRTRSWAVALKGLMLMHGFFLCKSTVAESIGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(17635. .17815,17901. .18019,18141. .18194,
18300. .18406,18547. .18611,18742. .18950))
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                                                                                                                                                              Hamilton News, S., Buehler, E., Chao, Q., Chin, C., Scheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Scheuk, R., Shinn, P., Brooks, S., Kim, C., Altafi, H., Bei, B., Chin, C., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, S., Mukharsky, N., Muyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. Direct Submitssion

NAL Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Bology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA

I. 132699

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RSLAIGETDA"
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                                                                                         Submitted (07-MAY-1999) Arabidopsis thaliana Genome Center, bepartment of Bloodgy, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 132699)
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      (bases 1 to 132699)
                               Ecker, J.R.
Direct Submission
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                   join(26661. .26948,27454. .27610,27713. .27814,27911. .28038,2834,22. .28470,28565. .28632,28747. .28969)
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                                                                                                                                                                                                                                                                             TPRRNSAGATNNDIMTTPRSYSSHRQNGYFKEVRRLSTAPLNFVAIPKEDSVSTYTSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota ngrajalantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Sosidae; eurosidas II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 1779)

Renard,M., Delourme,R., Barret,P., Brunel,D., Froger,N. and
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Gaps: 0
Percent Identity: 82.353
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Sequence 1 from Patent W00109356.
AX081276 AX081276.1 GI:13170125
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1. .1779
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Ratio: 4.118
Percent Similarity: 100.000
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Brassica napus
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GYGGYGYKSSEMAEVALKLEQLETWHGNAQEDGAHLATDTYHINPELYSMLDNML
TELAPPAATTGSNALNPEINNNNNEFTGGDLKAIGENAVCRRSNOPAFAVDSSSN
RLKPGSSPDGMYTSPSPAGVIGTTVTTVTGSTRPLILVDSQDNGVRLVHALMACAEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica napus
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids_II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutant gene of the gras family and plants with reduced development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1779)
Renard,M., Delourme,R., Barret,P., Brunel,D., Froger,N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      containing said mutant gene
Patent: WO 0109356-A 3 08-FEB-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 17
Gaps: 0
Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  455
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/db_xref="GI:13170128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AXO81278 1779 bp DNA Sequence 3 from Patent WO0109356. AXO81278
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1. .1779
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                                                                                                                                                                                                                                                                                                                                                                                                                                  476
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US-09-485-529-104 x AX081276
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Percent Similarity: 100.000
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seq_name: gb_pat:AX005809
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                                                                                                                   DEFINITION
ACCESSION
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ORIGIN
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AUTHORS
TITLE
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JOURNAL
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AUTHORS
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SOURCE
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                                                                                                                                                  VERSION
                                                                                                                                                                           SOURCE
NRFGSSGFAPAHLGSNAFKQASTLLALFNGGEGYRVEKNNGCLMLSWHTRPLITTSAW
                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Pooideae; Triticeae; Triticum.
1 (bases i to 200)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 69 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  24-AUG-2000
                                                                                                                                                                                                               7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 15
Gaps: 0
Percent Identity: 93.333
                                                                                            17
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                                                                                                                      Percent Identity: 76.471
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/db_xref="taxon:4565"
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                                                                                            Length:
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58 c 84 g 27 t
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172
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179
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185
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188
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                                                                                                                                                                                        Align seg 1/1 to: AX081278 from: 1 to: 1779
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                                                                                                                                                                                                                                                                                                                                                      AXUU5860 200 bp DNA
Sequence 69 from Patent WO9909174.
AXU05860
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                         430 c
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US-09-485-529-104 x AX081278
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US-09-485-529-104 x AX005860
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4.643
93.333
                                                                                                                     Percent Similarity: 100.000
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             KLSAVH
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LOCUS AX005860
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                         BASE COUNT
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AUTHORS
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                                       ORIGIN
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Enkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooleae; Triticeae; Triticum.

1 (bases 1 to 416)
Harberd, N. P. and Peng, J. Genetic control of plant growth and development Patent; WO 9909174-A 18 25-FEB-1999; HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Dalbergieae; Andira.

1 (bases 1 to 524)

Dutech,C., Ansellem,L., Billotte,N. and Jarne,P.

Characterization of (GA)n microsatellite loci using an enrichment protocol in the neotropical tree species Youacapoua americana
Unpublished
                       24 - AUG - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-FEB-2000
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Dutech,C., Amsellem,L., Billotte,N. and Jarne,P.
Direct Submission
Submitted (44-JAN-2000) CEFE, CNRS, 1919 route de Mende,
Montpellier cedex 05 34293, France
Location/Qualifiers
1.524
//organism="Andira aubletii"
//db_xref="taxon:115636"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
Locus AF224770 524 bp DNA Picrosatellite sequence.
DEFINITION Andira aubletii clone Bwa6-II microsatellite sequence.
ACCESSION AF224770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 13
Gaps: 0
Percent Identity: 100.000
                             PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Triticum aestivum"
/db_xref="taxon:4565"
168 c 129 g 60 t
     AAVUJ809 416 bp DNA
Sequence 18 from Patent WO9909174.
AX005809
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                                                                                                      AX005809.1 GI:9928806
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US-09-485-529-104 x AX005809
                                                                                                                                                                              Triticum aestivum
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Percent Similarity: 100.000
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seq_documentation_block:
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bread wheat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS AC015886 188716 bp DNA HTG 07-MAY-2001
DEFINITION Mus musculus clone CT7-378P20, WORKING DRAFT SEQUENCE, 26 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 188716) Birran, B., Linton, E., Nusbaum, C. and Lander, E. Mus musculus chromosome, clone CT7-378P20 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 7, 2001 this sequence version replaced gi:7230250.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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------- Project Information
Center project name: L737
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------ Summary Statistics
Sequencing vector: M13; M77815; 82% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 GACGGTCTCCTCGCGGCGCGGATACAAGGTCAGGTCGTCGGAGCTC 87
/clone="BwA6-II"
/note="Synonym: Vouacapoua americana"
                                                                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 62.500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AF224770 from: 1
                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                       108
                                                     1. .524 _ _ /note="microsatellite"
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AC015886.4 GI:13959257
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                     182
                                                                                                          /rpt_type=tandem
                                                                                                                                          /rpt_unit=ga
90 c
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                                                       repeat_region
                                                                                                                                                                                                                                                                                    alignment_scores:
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ORIGIN
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JOURNAL
REFERENCE
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JOURNAL
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AUTHORS
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KEYWORDS
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Sequencing vector: Plasmid; n/a; 18% of reads
Chemistry: Dye-primer-amersham; 84% of reads
Chemistry: Dye-primer-amersham; 84% of reads
Chemistry: Dye-terminator Big Dye; 16% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175387 bases at least Q40
Consensus quality: 184707 bases at least Q20
Insert size: 173000; agarose-fp
Insert size: 173000; agarose-fp
Insert size: 186216; sum-of-contigs
Quality coverage: 4.8 in Q20 bases.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pleces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1324 14.23.23; Cont. 9 of 123 bp in length 11424 112572; Cont. 9 of 1149 bp in length 11573 12672; gap of 100 bp 12673 12672; gap of 100 bp 12673 14167; Cont. 9 of 1495 bp in length 14168 14267; gap of 100 bp 14268 15746; Cont. 9 of 1479 bp in length 15747 1546; Cont. 9 of 1570 bp in length 15847 17416; Cont. 9 of 1283 bp in length 17517 17516; gap of 100 bp 18990 20317; Cont. 9 of 1283 bp in length 18900 20317; Cont. 9 of 1418 bp in length 18900 20317; Cont. 9 of 100 bp 20418 22468 22567; Cont. 9 of 2050 bp in length 22468 22567; Cont. 9 of 3253 bp in length 22568 25620; Cont. 9 of 3253 bp in length 2258
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151285 151384: gap of 100 bp
151385 188716: contig of 37332 bp in length.
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16554 bp in length
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118724 151284: contig of 32561 bp in length
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55425: contig of 10786 bp in length
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118623: contig of 32650 bp in length
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29289: contig of 3369 bp in length
889: gap of 100 bp
34348: contig of 4959 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1021 1120: gap of 100 bp 1121 2393: contig of 1273 bp in length 2394 2494 a 5699: contig of 1146 bp in length 3640 3739: gap of 100 bp 
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/db_xref="taxon:10090"
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8847: cor
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BAC"																								2502 others	
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misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	mișc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	BASE COUNT 52371	URIGIN

alignment_block:
US-09-485-529-104 x AC015886/rev ..
Align seg 1/1 to reverse of: AC015886 from: 1

to: 188716

seq_name: gb_pr:AL355796

United Submission

Submitted (13-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerques/Esanger.ac.uk

On Dec 24, 2000 this sequence version replaced gi:11990033.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation amnotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw., SWISSPROT; Tr., TREMBL; WP:, WORMPEP: Information on the WORWEPEP database can be found at IMPORTANT: This sequence is not the entire insert of clone RP11-46B11 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-46B11 is at 1 in this sequence. The true left end of clone RP3-50BD13 is at 151987 in this sequence. The true right end of clone RP11-454P17 is at 95829 in this http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping seq_documentation_block: LOCUS AL355796 152086 bp DNA PRI 23-DEC-2000 DEFINITION Human DNA sequence from clone RP11-46B11 on chromosome 6, complete Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RPI1-46B11 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 152086) http://www.chor1.org/bacpac/home.htm VECTOR: pBACe3.6 AL355796 AL355796.11 GI:11991379 Direct Submission Homo sapiens Almeida, J. sequence. sednence human. ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES COMMENT

3081. .4141 /note="LipBa repeat: matches -1537. .-412 of consensus" 4146. .7688 /note="LIPA13 repeat: matches 1832. .5346 of consensus" 7689. .7939 /note="11 repeat: matches 2364. .3549 of consensus" 1194. .1456 /note="1.1747 repeat: matches 5881. .6143 of consensus" 1457. .2384 182. .3056 'note="LIPBa repeat: matches -235. .1639 of consensus" /note="LiPA9 repeat: matches 5909. .6163 of consensus" 7940. .8737 Location/Qualifiers
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us-09-485-529-104.p2n.rge

15684. 15899

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//octe="L1 repeat: matches 4359. 4985 of consensus"
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/note="14 copies 2 mer ag 89% conserved" 14703. .14898
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#7010. .47938
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52035. .52143
/note="MIR repeat: matches 128. .236 of consensus"
53535. .53640
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53002. .55062
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49939. .50006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 3. .68 of consensus" 5007. .50317 /note="AluSx repeat: matches 1. .312 of consensus" 50318. .50406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="17 copies 2 mer aa 82% conserved"
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/note="MIR repeat: matches 4%. .252 of consensus"
57199. .57239
/note="20 copies 2 mer tt 95% conserved"
57862. .57977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60237. .60284
/note===24 copies 2 mer at 72% conserved"
60683. .60729
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Gaps: 0
Percent Identity: 56.250
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US-09-485-529-104 x AL355796/rev
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seq_name: gb_p1:AC007504

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join(6527. .6667,6772. .6859,7159. .7311,7597. .7757,
7840. .8514,8612. .8939,9020. .9240,9369. .9546,9658. .10142)
700ce="F13F21.2"
7note="Hypothetical Protein"
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SREEEDRSVRKRKRKRKRKPAKSEEKPKKKGGGFTKVCSLSPELQAFTGTPOLARTEVV
KMLMKYIKENNLODPSDKRTIICDESLRSLFPVESINMFOMNKOLAKHIMPLVQEDEA
COMPLEMENCKOKMKMETDEVKVNIKSSTFLNYIDNDESNEEKATSSRIKTEE"
/gene="F13F21.5"
complement(15762..16883)
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/db_xref="G1:5430747"

/db_xref="G1:54307
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NHRFVSGAEBEKVVRVPEAPLESFLKTLHITCAGGESFPEDLCADVQVLGANBALGLS
ONFYLLHSSEPLERKVVRPEAPLESFLKTHHITCAGGESFPEDLCADVQVLGANBALGLS
ONFYLLHSSEPLERWGGEGLJTFETVPEAAPAELKEPPIEDQLAFHTLWPESHKLY
GHGNELFSLCSDHKGNLVASSCKAQSASMAEIWHWEVGTWKAVGRLGSHSLTVTHLEF
SYDDTLLLSVSRDRHFSVFSIQTHUADROEVSHKLMAVKBAHKTINACSWANPFGHPRAT
SSRDKTVKINSVENDRIKGILVLPPFGSSYTAVAMTGLDNREKSGCVAVGNBSGLIE
LSNVKIIETEEGTTATAALALRLEPFWCHVSAVNRLAMRPTEKCESNQSLRMLTSCGD
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/podouc_=="geranyl pyrophosphate synthase"
/product=="geranyl gyrophosphate synthase"
/product=="geranyl gyrophosphate synthase"
/db_xref="dl:5430748"
/translation="mreystillsamelirpsonerlistensering your actions the product of the
                                                                                                                                                                                                                                                                                                                                                                                                                       WILKFEKYWEEYSDILAIAAVFDPRLKLKCLEYCFSTLDRLTSKSRLAHVRSKIYKLF
KAYKKRPSSITSSSQVETLEEDIPAGYSGFYAFVSQKVGSSGKSELDIYLGEPTLDMA
AFRHFNVLAYWKDNSCRFKELSSMACDVLSIPITTVASESSFSIGSGVLSKYRSSLLP
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AFVREQIDAFLESDALLESKPEQEEEDCNGDQNDEEGSENDDDKTELPVKAKKRGGGF
NKICQLSPQLEKFLGTSQLARTEVVKKWMAYIREHDLQDPTNRRNILCDESLHSLFRV
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                                                                                                                                                                                                                                                                                                                                                                     /translation="MTNLISGSSYPTANLYFMQVWKIECWLRAHEFSVDETICQMVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="97% identical to geranyl geranyl pyrophosphate synthase [Arabidopsis thaliana] g1[2578822."
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                                                  .4465,4631. .5020))
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                                                                                                                                                      /note="Hypothetical Protein"
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/gene="F13F21.4"
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/gene="F13F21.3"
complement(10370. .11380)
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/db_xref="G1:5430749"
                                                                                                                                                                                                                                                     /protein_id="AAD43146.1"
/db_xref="G1:5430746"
                                                  complement (join (4079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5527. .10142
/qene="F13F21.2"
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/gene="F13F21.4"
                                                                                              /gene="F13F21.1
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e-mail for correspondence: arabésequence.stanford.edu
Genes with similarity to proteins in the databases are described
as 'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compblo.ornl.gov/sectlon/index.hhml), GensSchN (chris Burge,
http://gnomic.stanford.edu/-chris/GENSCANW html), Fexa (V.Solovyev
& A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/),
NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/NetPlantGene.html) and
eMotifi(Nevill-Manning, C.G. Wu, T.D. & Brutlag, D.L.,
http://motif.stanford.edu/projects.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnollophyta; eudicotyledons; core eudicots; Spermatophyta; eucosids II; Brassicales; Brassicaceae; Arabidopsis. (bases 1 to 125021)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (06-MAY-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-JUN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Federspiel, N.A., Palm.C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P. Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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                                            AC007504 125021 bp DNA PLN 11-JUN-2001
Arabidopsis thaliana chromosome I BAC F13F21 genomic sequence,
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/db_xref="taxon:3702"
/chromosome="1"
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/clone="F13F21"
complement(4079. ,5020)
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                                                                                                                                                                 complete sequence.
seq_documentation_block:
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                                                                                         DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
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gene

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Oncomparison of the property o
                                                                                                                                                                                                                                                                                                                                                                          Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R.
High Throughput Mouse Sequencing
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 179481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Estimated insert size: agarose-FP - N/A
**Estimated insert size: 179221 - sum-of-contigs
Quality coverage: agarose-FP - N/A
Quality coverage: 9.4 x in Q20 bases; sum-of-contigs estimation
HTG 13-JUL-200.
14 clone RP23-46517 strain C57BL6/J,
14 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2: contig of 50762 bp in length
2: gap of unknown length
2: gap of unknown length
3: gap of unknown length
6: contig of 30174 bp in length
6: contig of 30174 bp in length
1: contig of 28595 bp in length
1: gap of unknown length
1: gap of unknown length
2: gap of unknown length
3: gap of unknown length
4: gap of unknown length
5: gap of unknown length
6: gap of unknown length
7: gap of unknown length
8: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bin'ws.exe/mouseDB/mouseSEQ/mouseseqtable.hts
Contact: htgs@sequence.aecom.yu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: puc18; L08752
Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 177183 at least Q20
*Consensus quality: 17458 at least Q30
*Consensus quality: 174495 at least Q30
Estimated insert size: agarose-FP - N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://sequence.aecom.yu.edu/cgi-
                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT. house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL
                                                      Mus musculus chromosome
                                                                                           WORKING DRAFT SEQUENCE,
                                                                                                                                                    AC034100.8 GI:14717146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50762:
                179481 bp
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122786:
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                                                                                                                                                                                                                                                          Mus musculus
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50783
92573
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122767
122787
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                           LOCUS
                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
REFERENCE
AUTHORS
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JOURNAL
                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                      KEYWORDS
SOURCE
                                                                                                                                                           VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AaD43153.1"
/db_xref="G1:5430753"
/translation="MQMDSAQNQFNKRARLFEDPELKDAKVIYPSNPESTEPVNKGYG
                                                                                                                                                    /protein_id="AaD43150.1"
/db_xref="G1:5430750"
/translation="MAMSHLFLSSSPQSSLALRLHSTTQFTLSYSKNNKDCSFQSANE
                                                                                                                                                                                                                                                AKVSKRSLLCRAIHMESGHSGEQPKKLNFDNILRRTKHVWDNSPOPVKEFPWNRAFGN
FOLVLLDLALSVKFLEVPILAVSSISEMSYCAHERKLALVPFPLVIGMVVAGYLQET
ALKISPRIKEAEVPPHIIAMMFFTLIKLPGPYYPWGRLLVPHFANGVLLRALWSMF
FWYKKTRNTSGNPLQNHSLETE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MERPFGCFFILLLISYTVVATFDDEPSFPENADLTKDLEGKCFS
INKVDPNLKFENDRLKRAYIALQAWKKAIYSDPFKTTANWVGSDVCSYNGVYCAPALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPPPVYSPPPPTFSPPPTHNTNQPPMGAPTPTGAPTPSSETTQVPTPSSESDQSQ1LS
PVQAPTPVQSSTPSSEPTQVPTPSSSESYQAPNLSPVQAPTPSSETSQVPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation-"mytlkmeiciellklitydfyaavaesievafrhrpppviqyssy
mygrrsnytavpiplygfl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDPYDASPVKNRRSPPPPKVEDTRVPPPQPPMSPSPSPPSP1XSPPPPVHSPPPPSSPPSSP
PPPPHVYSPPPPVASPPPPSPPPVHSPPVHSPPPPSPPSPPSPPSPPSPPSPPSPPSPPSPSP
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SSVPSSSPSTDTSIPPPENNDDDDDGDFVLPPHIGFQYASPPPPMFQGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="F13F21.6"
/note="University Location of ests 164G18T7
/gil2764114), 114G10T7 (gil2597578), and 114G11T7
(gil2597579)"
/codon_start=1
                                                      /note="Unknown Protein; Location of ests VBVQD12 (gil757594 and gil757593)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Join(28449, .28680,28766, .28965,29065, .29313)
/gene="Fl3F21.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AC007504 from: 1 to: 125021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Hypothetical Protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAD43151.1"
/db_xref="G1:5430751"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAD43152.1"
/db_xref="G1:5430752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Unknown Protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23803. .26346
/gene="F13F21.7"
23803. .26346
/gene="F13F21.7"
                                                                                                                                                                                                                                                                                                                                                                                    21730. .21921
/gene="F13F21.6"
21730. .21921
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                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-485-529-104 x AC007504/rev
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Ratio: 3.615
Percent Similarity: 100.000
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contig of 202 bp in length gap of unknown length contig of 199 bp in length

177244: 177045:

177025

176824 177026 177046

seq_name: gb_htg:AC034100 seq_documentation_block:

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/codon_start=1
                                                                                                                                                                                                 (bases 1 to 329709)
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Mesorhizobium loti
                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                   Kaneko, T.
                                                                                                                                                                                      21082930
 ORGANISM
                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AP002997 329709 bp DNA BCT 15-MAY-2001
Mesorhizoblum loti DNA, complete genome, section 4/21.
AP002997 BA000012
AP002997.2 GI:14022051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 others
177264: gap of unknown length
178663: contig of 1399 bp in length
178683: gap of unknown length
179208: contig of 525 bp in length
179228: gap of unknown length
179481: contig of 253 bp in length.
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Mesorhizobium loti (strain:MAFF303099) DNA
                                                                                                                                                                                                                                                                                                                                                                                                           Vector_side.left"
168088. .174488
/note="assembly_name:Contig93"
174509. .175363.
/note="assembly_name:Contig92"
175384. .175665.
/note="assembly_name:Contig90"
175686. .176603
/note="assembly_name:Contig90"
176824. .177025
/note="assembly_name:Contig89"
177046. .177244
/note="assembly_name:Contig88"
177068. .178684. .179248
/note="assembly_name:Contig88"
177265. .178663
/note="assembly_name:Contig86"
179229. .179481
/note="assembly_name:Contig86"
179229. .179481
                                                                                                                                                                                                                            /note="assembly_name:Contig98"
50783. .92572
/note="assembly_name:Contig97"
92593. .122766
/note="assembly_name:Contig96"
122787. .151381
                                                                                                                                                                                                                                                                                                                                                      vector_side:right"
151402. .168067
/note="assembly_name:Contig94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AC034100 from: 1 to: 179481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                           1. .179481
/organism="Mus musculus"
/organi="C5PL6/J"
/db_xref="taxon:10090"
/chromosome="14"
/clone="RP23-46517"
                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                        clone_end:T7
                                                                                                                                                                                                    /sex="male"
                                                                                                        179481
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US-09-485-529-104 x AC034100
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3.917
85.714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
Locus AP002997 3
                           178664
178684
179209
179229
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Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti

DNA Res. 7 (6), 331-338 (2000)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; Yana 1532-3; Kisarazu, Chiba 292-0812, Japan (E-mail: kaneko@kazusa.or.jp, Thizobase/, Tal: http://www.kazusa.or.jp/rhizobase/, Tel: 81-438-52-3935(ex.2338), Fax:81-438-52-3934)
On May 11, 2001 this sequence version replaced g1:11994965.
Location/Qualifiers
1. 329709
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CDS

CDS

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                                                                                                                                protein of ABC transporter"
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Gaps: 0
Percent Identity: 62.500
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Sequence 64 from Patent W09909174.
AX005855
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Triticum aestivum
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ACCESSION
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KEYWORDS
CDS
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complement(7153..7956)
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CDS

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VSESESTKRQDMYTPIMPLVVDPNKSQSKPLALEQKNNNDQIINNQAESHSVSSSNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STNSNI SFFEKFKQFFSKQKKKNI SSQHEQEQTKA I HQESQQI DSRELNENEQSEPFI
DFGSTILDSVASNY I DSKA EYENSTNI AASYNTQDI QVKQQEFDPSEASEPI DI GNTK
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                                                                                              2 (bases 1 to 312430)
Andersson.A.G.E.
Direct Submission
Submitted (11-NOV-1998) S.G.E. Andersson,
Siv.Andersson@molbio.uu.se, Dept. of Molecular Biology, University
of Uppsala, Husargatan 3, Uppsala, S-751 24, SWEDEN
On NOV 13, 1998 this sequence version replaced 91:3860788.
  The genome sequence of Rickettsia prowazekii and the origin of mitochondria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="TAIL-SPECIFIC PROTEASE PRECURSOR (ctp)"
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    .312430
    /organism="Rickettsia prowazekii"
/strain="Madrid E"

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                                                                                                                                                    TITLE
JOURNAL
                                                                                                   REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                               FEATURES
       TITLE
                                                                                                                                                                                                                                                        COMMENT
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticum.

1 (bases 1 to 309)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 64 25-FEB-1999;
HARBERD NICHOLAS FAUL (GB); PENG JINRONG (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPXX02 312430 bp DNA BCT 12-NOV-1998 Rickettsia prowazekii strain Madrid E, complete genome; segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ35271 AJ235269
AJ235271.1 GI:3868717
Complete genome.
Rickettsia prowazekii.
Rickettsia prowazekii.
Rickettsia prowazekii.
Rickettsia prowazekii.
I (bases 1 to 312430)
Andersson, S.G., Zomorodipour, A., Andersson, J.O.,
Sicheritz-Ponten, T., Alsmark, U.C., Podowski, R.M., Naslund, A.K.,
Eriksson, A.S., Winkler, H.H. and Kurland, C.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 9
Gaps: 0
Percent Identity: 100.000
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102 c 102 g 45 t
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95
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US-09-485-529-104 x AX005855
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Percent Similarity: 100.000
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SOURCE
ORGANISM
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ORIGIN
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                                                                                                                             TITLE
JOURNAL
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gene

CDS

gene

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10753. .11238
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Molecular cloning of the full-length cDNA of (S)-hydroxynitrile
lyase from Hevea brasiliensis. Functional expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                 NAIARVWLKVGKGKIVVNNKILNQYFPSETYVKTILQPFILTKTIDQYDVICTVKGG
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1 (bases 1 to 1078)
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Gaps: 0
Percent Identity: 60.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="tRNA Met (CAT)"
complement(12284. 12769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(12284. .12769)
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11279. .11352
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US-09-485-529-104 x RPXX02
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WSYNLSKHKKNNYIGGGILHHNGKLXITYGARLLIVLDAKSGYEIIRKELPDIIRIKP
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191 c 239 g 324 t
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( bases 1 to 1091)

Hasslacher, M., Schall, M., Schwab, H., Hayn, E.M., Kohlwein, S. and
coli and Saccharomyces cerevisiae and identification of an active
                                                                    2 (bases 1 to 1078)
Hasslacher, M., Schall, M., Hayn, M., Griengl, H., Kohlwein, S.D. and
                                                                                                                                           Submitted (09-NOV-1995) Meinhard Hasslacher, Department of Biochemistry, University of Technology Graz, Petersgasse 12/2, Graz, 8010, Austria
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(S)-HYDROXYNITRILLYASE FROM HEVEA BRASILIENSIS
Patent: WO 9703204-A 1 30-JAN-1997;
DSM CHEMIE LINZ GMBH (AT)
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Gaps: 0
Percent Identity: 66.667
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Sequence 1 from Patent W09703204.
A59586
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Hevea brasiliensis
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                    site residue
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 161592)
2 (bases 1 to 161592)
2 (bases 1 to 16192)
2 (cox, C., Davis, C., Dalgado, O., Ding, Y., Dugan-Rocha, C., Brown, J., Buhay, C., Davis, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R., Massey, E., McLeod, M.P., Mel, G., Moore, S., Morgan, M., Parish, B., Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S., Wuzly, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G., Worley, K. and Gibbs, R.
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Worley, K.C.

Direct Submission

Submitted (22-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 4, 2000 this sequence version replaced gl:8248608.

Center: Baylor College of Medicine

Center: Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC026377 161592 bp DNA HTG 06-NOV-2000 Mus musculus chromosome 11 clone RP23-267J8, *** SEQUENCING IN PROGRESS ***, 64 unordered pieces.
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                                                                                                                                                                                                   Length: 15
Gaps: 0
Percent Identity: 66.667
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                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                 Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1.8x in Q20 bases; sum-of-contigs estimation
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in length

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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 96065: contig of 28600 bp in length

166 96165: gap of unknown length

166 129939: contig of 33774 bp in length

140 130039: gap of unknown length

172569: contig of 42530 bp in length

17269: gap of unknown length

17269: gap of unknown length

17269: contig of 41936 bp in length

17260: contig of 41936 bp in length.
                                                                                                                                                                                                6649: contig of 3526 bp in length.
6749: gap of unknown length.
12672: contig of 5823 bp in length.
12672: gap of unknown length.
18722: contig of 6050 bp in length.
18822: gap of unknown length.
26781: contig of 7959 bp in length.
2681: gap of unknown length.
2681: gap of unknown length.
                                                                                                                                                  3023: contig of 3023 bp in length
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    214605
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6750. .12572
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-MAY-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is not known and their order in the contigs are represented as arbitrary. Gaps between the contigs are represented as
                                                             6390 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: NIH Intramural Sequencing Center Center code: NISC
Web site: http://www.nisc.nih.gov
Centact: nisc_mouse@nhgri.nih.gov
Center project Information
Center project name: cgo
Center clone name: 494009
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                              Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                       to: 161592
                                /clone="RP23-267J8"
40073 a 36398 c 37212 g 41519 t
                                                                                                                                                                                                                                      Gaps:
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HTG; HTGS_PHASE1; HTGS_DRAFT
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3.462
86.667
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US-09-485-529-104 x AC026377
                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AC026377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_htg:AC091618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green, E.D.
                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                            alignment_scores:
                                                             BASE COUNT
ORIGIN
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AUTHORS
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JOURNAL
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
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SOURCE

1027 others

us-09-485-529-104.p2n.rge

ACCESSION KEYWORDS SOURCE

VERSION

REFERENCE

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50171 50270: gap of 100 bp 54191 50270: gap of 1320 bp in length 54291 58991: contig of 3920 bp in length 54291 58991: contig of 4601 bp in length 58992 94581: contig of 35590 bp in length 94582 94681: contig of 35590 bp in length 94582 94681: contig of 41024 bp in length 135706 135805: gap of 100 bp 135806 175324: contig of 39519 bp in length 175325 175424: gap of 100 bp 175425 228201: contig of 52777 bp in length.
23 36322; gap of 100 bp 3686; contig of 664 bp in length 87 37086; contig of 680 bp in length 67 3786; gap of 100 bp 67 44313; contig of 647 bp in length 14 4413; gap of 100 bp 114 4513; gap of 100 bp 12 50170; contig of 5757 bp in length 14 50170; contig of 5757 bp in length 14 50170; contig of 5757 bp in length 15 50170; contig of 5
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86.667 Percent Identity: 66.667
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52016 c 52776 g 62491 t
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54291. 58891
/note="assembly_fragment"
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/note="assembly_fragment"
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37087. .37766
/note="assembly_fragment"
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/note="assembly_fragment"
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94682. 135705
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/note="assembly_fragment"
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/note="assembly_fragment"
36323. .36986

    .35674
    /note="assembly_fragment clone_end:SP6 vector_side:left"

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/clone="RP23-2M16"
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US-09-485-529-104 x AC016814/rev
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                                                                                                                                                                                                                                   AC016814 228201 bp DNA HTG 13-MAY-2001
Mus musculus clone RP23-2M16, WORKING DRAFT SEQUENCE, 12 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 228201)
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 2_M_16

Center clone name: 2_M_16

Sequencing vector: M13, M77815; 16% of reads
Sequencing vector: M13, M77815; 16% of reads
Sequencing vector: Plasmid; n/a; 84% of reads
Sequencing vector: Plasmid; n/a; 84% of reads
Sequencing vector: Plasmid; n/a; 84% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 224356 bases at least 030
Consensus quality: 22619 bases at least 030
Consensus quality: 226246 bases at least 020
Insert size: 217100; sum-of-contigs
Insert size: 227101; sum-of-contigs
Quality coverage: 20.7 in 020 bases; agarose-fp
Quality coverage: 20.7 in 020 bases; agarose-fp
Quality coverage: 20.7 in 020 bases; agarose-fp
Quality soverage: 20.7 in 020 bases; agarose-fp
Quality coverage: 20.7 in fall sequence record is
** is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus chromosome, clone RP23-2M16
           206262 GATGAGTTCCCGGCCAGCTTAGGTTACAAGGTGAGATCT 206224
                                                                                                                                                                                                                                                                                                                                                                                        AC016814.6 GI:14030018
HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                seq_documentation_block:
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TITLE
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COMMENT

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f unknown length
g of 1205 bp in length
f unknown length
g of 1275 bp in length
unknown length
g of 1177 bp in length
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g of 1309 bp in length
f unknown length
g of 1150 bp in length
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of 1078 bp in length
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LOCUS AC020887 271519 bp DNA HTG 29-MAR-2000
DEFINITION MUS musculus clone RP23-472H3, WORKING DRAFT SEQUENCE, 86 unordered
                                                                                                                                                                 Web site: http://www.jgi.doe.gov
-----Summary Statistics
Consensus quality: 168487 bases at least Q40
Consensus quality: 2137951 bases at least Q30
Consensus quality: 213703 bases at least Q20
Estimated insert size: 271519; sum-of-configs estimation
Estimated insert size: 255000; pulse field gel estimation
Quality coverage: 3.76x in Q20 bases; pulse field gel estimation
Quality coverage: 2.84x in Q20 bases; sum-of-contigs estimation
                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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seq_name: gb_htg:AC070284

Unpublished

2 (bases 1 to 878)

Estain.No., Morrison,H.G., McArthur,A.G., Nixon,J., Kim,U.,
Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L.
Direct Submission

L. Submitted (06-JUN-2000) Josephine Bay Paul Center for Comparative
Molecular Biology and Evolution, Marine Biological Laboratory, 7

MBL Street, Woods Hole, MA 02543-1015, USA

* NOTE: This record contains 1 individual

* Sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will seq_documentation_block: LOCUS AF090137 1241 bp mRNA PRI 12-MAR-1999 DEFINITION Homo sapiens carbohydrate sulfotransferase 1 (CHST1) mRNA, complete Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1241)
Li,X. and Tedder,T.F. AC070284 878 bp DNA HTG 06-JUN-2000 Giardia intestinalis clone EJ6500 strain WB-C6, LOW-PASS SEQUENCE 1 (bases 1 to 878) Morrison, H.G., McArthur, A.G., Nixon, J., Eakin, N.Q., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L. Giardia: a model for ancient eukaryotic genome analysis Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia. 4 others 1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16 878: contig of 878 bp in length Jenyth: 16 Gaps: 0 Percent Identity: 43.750 /organism="Giardia intestinalis" ų 198 from: 1 to: 878 /db_xref="taxon:5741" /clone="EJ6500" 197 c 244 g Location/Qualifiers 1. .878 /strain="WB-C6" AC070284.1 GI:8272795 HTG; HTGS_PHASE0. Giardia intestinalis. Giardia intestinalis AF090137 AF090137.1 GI:4406151 44.00 3.143 87.500 alignment_block: US-09-485-529-104 x AC070284 Align seg 1/1 to: AC070284 preserved. seq_documentation_block: LOCUS AC070284 DEFINITION Giardia integ seq_name: gb_pr:AF090137 SAMPLING. Quality: Ratio: Percent Similarity: 235 human. alignment_scores VERSION KEYWORDS SOURCE ORGANISM source DEFINITION ORGANISM BASE COUNT ORIGIN TITLE JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS TITLE JOURNAL ACCESSION ACCESSION REFERENCE AUTHORS VERSION KEYWORDS SOURCE FEATURES COMMENT

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Bacillus subtilis.
Bacillus subtilis.
Bacillus subtilis
Bacteria, Firmicutes, Bacillus/Clostridium group;
Bacillus/Faphylococcus group; Bacillus/Eaphylococcus group;
Bacillus/Eaphylococcus group;
Bacillus/Eaphylococcus group;
Bacillus/Eaphylococcus group;
Marasco,R., Varcamonti,M., Ricca,E. and Sacco,M.
A new Bacillus subtilis gene with homology to Escherichia coli pro Gene 183 (1-2), 149-152 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-1997
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Submitted (06-JUN-1996) M. Sacco, Istituto Internazionale di
Genetica e Biofisica, via Marconi 10, 80125, Napoli ITALY
Location/Qualifiers
                                                                                                                                                                                       /product-'keratan sulphate
6-sulfo-transferase'
R 1237 .1458.
Location/Qualifiers
(C12N15/09,C12R1:19);
strandedness: Single;
tropology: Linear;
hypothetical: No;
anti-sense: No;
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                                                                                                                                    /organism='Homo sapi/tissue_type='Brain'
                                                                                       Location/Qualifiers

    .2096
    /organism="Bacillus subtilis"

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/db_xref="taxon:9606"
a 526 c 421 g 25
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535. .540
558. .563
570. .1992
592. .1992
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/gene="orfRM1"
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-10_signal
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FRTGKSRADARNAMGASRDLLRSLYDCDLYFLEBNIYRPPRVHHTDRIFRRGASRYL
CSRPVCDPPGPADLVLEEGDCVRKCGLLNLTVAABACRERSHVAIKTVRVPEVNDLRA
LVEDPRLNLKYIQLYRPROTILASRSFTFRDTYRLRRLMYGTGRKPYNLDVTQLTTVC
EDFSNSVSTGLMRPPWLKGKYMLVRYEDLARNPMKKTEEIYGFLGIPLDSHVARWIQN
NTKGDPTGSRKYGTYRNSAATAEKWRFRLSYDIVAFAQNACQQVLAQLGYKIAASEE
EKNRSVSLVEERDFFFS"
197 t
                                                                                                                     Direct Submission
Submitted (03-SEP-1998) Immunology, Duke University Medical Center,
Durham, NC 27710, USA
                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MQCSWKAVLLLALASIAIQYTAIRTFTAKSFHTCPGLAEAGLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1458)
Fukuda,M. and Hanebuchi,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KERATAN SULPATE 6-SULFOTRANSFERASE AND DNA CODING FOR THE SAME Datent: JP 1998155488-A 1 16-JUN-1998;
SETRAGAKU KGGYO CO LTD
OS Homo sapiens (human)
N JP 1998155488-A/1
PD 16-JUN-1998
PF 29-NOV-1996 JP 1996320535
PI FUKUDA MASARAZU, HANEBGCHI NAGAMOTO
PC C12N15/09; CO7P121/04, CO7K14/47, C08B37/00, C12N9/10, PC C12P19/26//C12P21/02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-1999
 CHST1 and CHST2 sulfotransferases expressed by human vascular endothelial cells: cDNA cloning, expression, and chromosomal
                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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                                                                                                                                                                                                                                           /tissue_type="umbilical vein endothelium"
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Percent Identity: 57.143
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    1241
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                                                 Genomics 55 (3), 345-347 (1999)
99168906
                                                                                                                                                                            Location/Qualiflers
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E16306.1 GI:5710989
JP 1998155488-A/1.
Homo sapiens.
                                                                                     2 (bases 1 to 1241)
Li,x. and Tedder,T.F.
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Percent Similarity:
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RFTQGKSPADRRVMLGASRDLLRSLYDCDLYFLENYIKPPPVNHTTDRIFRRGASRVL
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LOCUS AB003791
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STVKLTVARMLTADGEWIHKKGIRPQVKAELPBSNVPLIGETTFGKGTVQTAREXDDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (30-JUL-1996) Medicine, Thomas Jefferson University, 1020 Locust Street, Philadelphia, PA 19107-6799, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"part of the sequence corresponds to an EST, GenBank
Accession Number R16177, which is similar to the chicken
chondroitin-6-sulfotransferase cDNA sequence, GenBank
Accession Number D49915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation-"MQCSWKAVLLIALASIAIQYTAIRTFTAKSFHTCPGLAEAGLAE
RLCEESPTFAYNLSRKTHILILATTRSGSSFVGQLFNQHLDVFYLFEPLYHVQNTLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mazany, K.D., Peng, T., Watson, C.E., Tabas, I. and Williams, K.J.
Human chondroitin 6-sulfotransferase: cloning, gene structure, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2190)
Williams K.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSU65637 2190 bp mRNA PRI 06-AUG-1998
Homo sapiens chondroitin-6-sulfotransferase mRNA, complete cds.
U65637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="chondroitin-6-sulfotransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Atherosclerosis: cell biology and lipoproteins Curr. Opin. Lipidol. 7 (6), U202-U208 (1996) 97189336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosomal localization
Biochim. Biophys. Acta 1407 (1), 92-97 (1998)
98306085
                                                                                                                                                                                                                                                                                                                                                        44.00 Length: . 15
3.143 Gaps: 0
93.333 Percent Identity: 53.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 2190)
Peng,T., Tabas,I. and Williams,K.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 2096
                                                                                                                                                                                                                                                    494
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                  482 g
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                                                                                                                                                                                                                                   2018
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US-09-485-529-104 x BSORFRM1
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SOURCE
ORGANISM
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VERSION
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AUTHORS
TITLE
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JOURNAL
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/trainiation="MQCSWKAVLLLALASIAIQYTAIRTFTAKSFHTCPGLAEAGLAE
RLCEESPTPAKNLSRKTHILILATTREGSSFWGQLFWQHLDVEYLFEPLYHVONTLIP
RFTGGKSPADRRWLGASRDLLRSLYDCDLYFLENT IKPPFVNHTTDRIFRGASRVL
CSRPWCDPPGPADLVLEEGDCVRKGGLLNLYVAAEACRERSHYAIRTWRVPEYNDLRA
LVEDPRLNIKYIQLVRDPRGILASRESTFRDTYRLWRLWYGGGKRPYNLDVTQLTTVC
EDFSNSVSYGTGLMRPWLKGKYMLVRYEDLARNPWKTFEIIGFIGIPLDSHVARHIQN
RTGDPTLGKHKYGYRNRSAATAEKWRRFLSYDIVAFAQNACQOVLAQLGYKIAASEE
ELKNPSVSLVEERDFFRFS
                      LVEDPRLNLKVIQLVRDPRGILASRSETFRDTYRLWRLWYGTGRKPYNLDVTQLTTVC
EDFSNSVSTGLMRPPWLKGKYMLVRYEDLARNPWKKTEEIYGFLGIPLDSHVARWIQN
NTRGDPTLGKHKYGTVRNSAATAEKWRFRLSYDIVAFAQNACQQVLAQLGYKIAASEE
CSRPVCDPPGPADLVLEEGDCVRKCGLLNLTVAAEACRERSHVAIKTVRVPEVNDLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-MAY-1997) to the DDBJ/EMBL/GenBank databases. Osami Habuchi, Aichi University of Education, Department of Life Science, Igaye-cho, Kariya, Aichi 448, Japan (Tel:0556-36-3111, Fax:0556-36-437)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular cloning and characterization of human keratan sulfate Gal-6-sulfotransferase J. Biol. Chem. 272 (51), 32321-32328 (1997) 98070405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABO03791 2415 bp mRNA PRI 14-FEB-1998 Homo sapiens mRNA for keratan sulfate Gal-6-sulfotransferase, complete cds.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (sites)
Fukuta,M., Inazawa,J., Torii,T., Tsuzuki,K., Shimada,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 14
Gaps: 0
Percent Identity: 57.143
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keratan sulfate Gal-6-sulfotransferase
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Homo sapiens
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/organism="Homo sapiens"
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/chromosome="11"
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/map="lp11.1-11.2"
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367. .1602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 2190
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/db_xref="GI:2887403"
                                                                                                         ELKNPSVSLVEERDFRPFS"
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                                                                                                                                  717 c
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Direct Submission
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US-09-485-529-104 x HSU65637
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alignment_scores
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LASCDRSTPAIVRWFAANLLYELACAEEHLPSYVLNCCHDLLVTQSGAVTKRGGLSSG
DPITSVSNTIYSLVIYAQHMVLSYFKSGHPHGLLFLQDQLKFEDMLKVQPLIVYSDDL
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CPGKNSFLDEAAYCNHLDVLRLLSKTTLTCLGDFKQLHPVGFDSHCYVFDIMPQTQLK
TIWRFGQNICDAIQPDYRDKLMSMVNTTRVTHVEKPVRYGQVLTPYHRDREDDAITID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="LAASGLTRCGRGGLVVTETAVKIVKFHNRTFTLGPVNLKVASEV
ELKDAVEHNQHPVARPIDGGVVLLRSAVPSLIDVLISGADASPKLLAHHGPGNTGIDG
TLWDFESEATKEEVALSAQIIQACDIRRGDAPEIGLPYKLYPVRGNPERVKGVLQNTR
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LDSRPDCPRQLTEHGCEDAALKDLSKYDLSTQGFVLPGVLRLVRKYLFAHVGKCPPVH
RPSTYPAKNSMAGINGNRFPTKDIQSVPEIDVLCAQAVRENWQTVTPCTLKKQYCGKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases I to 4374)
Butlista, b.M. and McGruder, E.D.
Direct Submissel, b.M. and McGruder, E.D.
Direct Submissel, b.M. and Development, Elanco
Submitted (23-AUG-2000) Biology Research and Development, Elanco
Animal Health, a Division of Eli Lilly and Company, 2001 West Main
St, Greenfield, IN 46440, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLYAESPTMPNYHWWVEHLNLMLGFQTDPKKTAITDSPSFLGCRIINGRQLVPNRDRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porcine reproductive and respiratory syndrome virus. Porcine reproductive and respiratory syndrome virus viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales; Arteriviridae; Arterivirus.

1 (bases 1 to 4374)

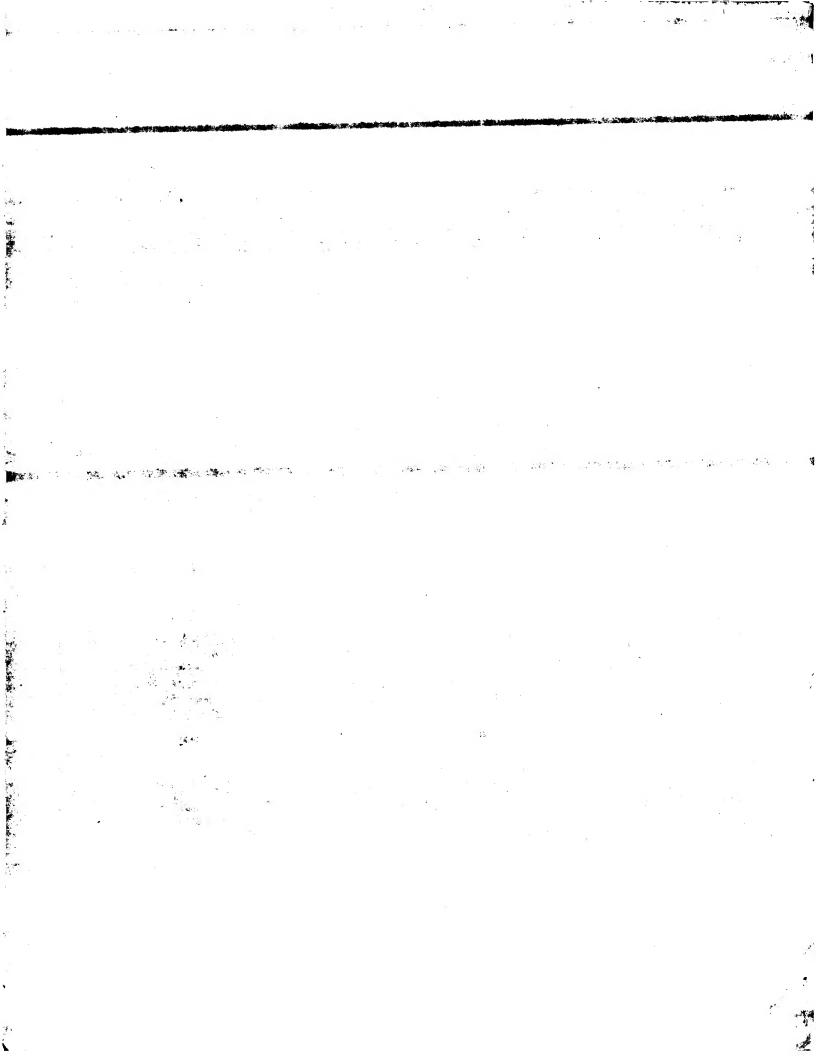
2 (bases 1 to 4374)

Cloning and expression of PRRSV ORFIb and demonstration and characterization of its NTPase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF298771 4374 bp RNA VRL 09-OCT-2000 Porcine reproductive and respiratory syndrome virus RNA-dependent

    .4374
/organism="Porcine reproductive and respiratory syndrome

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/note="ORFlb; zinc-finger protein; helicase (NTPase);
expression of ORFlb occurs due to an upstream ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="RNA-dependent RNA polymerase"
/protein_id="AAG22078.1"
/db_xref="G1:10719656"
                                                                                                                                                                                                                                                                                                                                                                                                                            1498 CAGGTGCTGGCCCAGCTGGGCTACAAGATCGCCGCCTCGGAG 1539
                                                                                                                                                                     Gaps: 0
Percent Identity: 57.143
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                                                                                                                                                                                                                                                                                                                                      to: 2415
  486
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<1. 4374
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     687
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US-09-485-529-104 x AB003791
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LOCUS AF298771
DEFINITION POrcine repro
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                                                                                                                                         Quality:
Ratio:
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  437
                                                                                                                  alignment_scores
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BASE COUNT
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REFERENCE
AUTHORS
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TITLE
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JOURNAL
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KEYWORDS
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GAGYMYGPSYPLGTPOVYSYLTKFYKGEAQLLPETYFSTGRIEVDCREYLDDREREV
AASLPHAFTGDVKGTTVGGCHHYTERLPRYLPKESYAVOYSSPGKAAKALCTIDV
YLPDLEAYLHPETGSKCWKMLDFKERVLMYWKDKTAYFQLEGRYFTWYQLASYASYI
RVPYNSTYYLDDCWAPALCHRRYVGSTHWGADLAYTPDYGAKI ILSSAYHGENPPSY
KILACAEFSLDDPVKYKHTWGFESDTAYLXEFTGNGEDWEDYNDAFRARQEGKIYKAT
SSQGATFDVYTLHLPTKDSLNRQRALVAITRARHAIFVYDPHRQLQGFFDLPAKGTPV
NLAVHRDGQLIVLDRNNKECTVAQALGNGDKFRATDKRVVDSLRAICADLEGSSSSPLP
KVAHNLGFYFSPDLTQFAKLPVELAPHWPVVTTQNNEKWPDRLVASLRPIHKYSRACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 17
Gaps: 0
Percent Identity: 47.059
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2.750
94.118
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US-09-485-529-104 x AF298771
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CEEPV spheroidin.
CfEPV spheroidin.
Protein encoded by
Protein encoded by
Escherichia coli p
Neisseria meningit
Neisseria meningit
S. epidermidis ope
S. epidermidis ope
Pseudomonas aerugi
Arabidopsis thalia
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Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
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            Arabidopsis thalia
Arabidopsis SCLa8.
A. thaliana transc
Arabidopsis thalia
                                                               Amino acid séquenc
Amino acid sequenc
                                                                                                                   Hevea brasiliensis
Keratan sulphate 6
                                                                                         Protein encoded by
                                                                                                        Hevea brasiliensis
thalia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
paclobutrazol.
Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide derived from a protein causing growth inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                           AAB82666
AAG44380
AAG4838
AAG43311
AAG43313
AAG43310
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AAG43310
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AAY30180
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AAY74417
AAY74418
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AAG82648
AAG82648
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AAG29564
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AAM40727
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AAE02560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY02537 standard; Peptide;
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WPI; 1999-181040/15
W09909174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-1998;
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 AAY02537
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Protein encoded by
Arabidopsis thalia
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Arabidopsis SCLa2.
Arabidopsis thalia
A. thaliana transc
                                                                                                        (without alignments)
52.688 Million cell updates/sec
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                                                                                         ; Search time 23.9 Seconds
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                hits satisfying chosen parameters:
                                                                                                                                                                                                                                    522463 seqs, 74073290 residues
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                                                                                         December 19, 2001, 17:03:44
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Maximum Match 100%
Listing first 45 summaries
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AAY02538
AAY02541
AAG38577
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AAB28575
AAW30792
AAE02545

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                     DELLAALGYKVRASDMA
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81
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Maximum DB seq length: 200000000
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                                   The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth inhibition is antagonised by globerellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with globerellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being globerellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit globerellin blosynthesis, such as pacloburrazol, e.g. to allow use of a globerellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents
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Claim 1; Page 53; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DELLAALGYKVRASDMA 17
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N-PSDB; AAX36279.
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Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                         17 AA;
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expressed
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used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by the wheat Rht clone 5al genomic sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 623;
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100.0%; Pred. No. 1e-06;
.ive 0; Mismatches 0; Indels
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Matches 17; Conservative
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Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; rice; expressed sequence tag; EST.

97GB-0017192.

13-AUG-1997; 07-AUG-1998;

WO9909174-A1.

25-FEB-1999

Protein encoded by rice EST D39460 sequence.

(first entry)

16-JUL-1999

AAY02538;

AAY02538 standard; Protein; 256 AA.

AAY02538

RESULT

22 dellaalgykvrssdma 38

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100 AA

Sequence

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence is encoded by the partial sequence of the maize D8-2023 allele.
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Score 78; DB 20; Length 100;
Pred. No. 4.7e-07;
1; Mismatches 0; Indels
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                                                                                                                                        1 DELLAALGYKVRASDMA 17
                                                                      16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   paclobutrazol; maize.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-181040/15.
                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX36282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX02543;
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays
                                                                      Matches
                                                                                                                                                                                                                                                                                                                      RESULT
AAYO2543

ID AAYO2543

XX AAYO2
XX AAYO2
XX AAYO2
XX AAYO2
XX RW ANTA
XX BAL AAYO2
XX BAL
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence is encoded by the expressed sequence tag (EST) AAD39460, which is homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 78; DB 20; L
Pred. No. 1.4e-06;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY02541 standard; Protein; 630 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Fig 6b; 88pp; English.
                                                                                                                                                                                                                                                                                                                 (PLAN-) PLANT BIOSCIENCE LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 96.3
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                  Peng J,
                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-181040/15.
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ID AAY0
XX
AC AAY0
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Gaps

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Indels

; 0

Mismatches

Query Match 96.3%; Best Local Similarity 94.1%; Matches 16; Conservative

DELLAALGYKVRASDMA 17

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Score 78; DB 20; Length 123; Pred. No. 6e-07;

Zea mays.

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990S-0132486-
990S-0132863-
990S-0132863-
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990S-0134218-
990S-0134218-
990S-0134768-
990S-0134941-
990S-0134941-
990S-0135523-
990S-0135523-
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990S-0137528.
990S-0137724.
990S-0138094.
990S-0138847.
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99US-0127462.
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99US-0128714.
99US-0129845.
99US-0130077.
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99US-0139458.
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                                                                                 2000EP-0301439
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99US-0139463
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99US-0139817
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                    28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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10-JUN-1999;
10-JUN-1999;
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16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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14 -MAY -1999;
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14-MAY-1999;
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18-JUN-1999;
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14-MAY-1999;
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28-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by plants. The products can be used to provide Rht expression in blants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by the maize lal genomic clone sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                            Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
paclobutrazol; maize.
                                                                                                                                                                                                                                                                                                                                                         New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.3%; Score 78; DB 20; Length 630; 94.1%; Pred. No. 3.8e-06; Indels 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 47612.
                                      Protein encoded by maize lal genomic clone sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG38577 standard; Protein; 517 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 9b; 88pp; English.
                                                                                                                                                                                                                                                              (PLAN-), PLANT BIOSCIENCE LTD.
                                                                                                                                                                                                         98WO-GB02383.
                                                                                                                                                                                                                                   97GB-0017192.
           16-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                 WPI; 1999-181040/15.
N-PSDB; AAX36280.
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                                                                                                                                                   W09909174-A1
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                                                                                                                                                                              25-FEB-1999
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99US-0140991

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

AAG38577;

ò a AAG38577
XX
XX
AC AAG3
XX
DT 18-C
XX
XX
DE Arab
XX
KW Prot
KW hybi
XX
C

15-SEP-1999;
20-SEP-1999;
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17-CCT-1999;
17-CC

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99US-0147935
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99US-0148319
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99US-0151065
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30 - 704 - 1999; 01 - 704 - 1999; 06 - 704 - 1999; 06 - 704 - 1999; 06 - 704 - 1999; 06 - 704 - 1999; 06 - 704 - 1999; 13 - 704 - 1999; 13 - 704 - 1999; 16 - 704 - 1999; 16 - 704 - 1999; 16 - 704 - 1999; 17 - 704 - 1999; 18 - 704 - 1999; 18 - 704 - 1999; 19 - 704 - 1999; 22 - 704 - 1999; 23 - 704 - 1999; 23 - 704 - 1999; 24 - 704 - 1999; 25 - 704 - 1999; 26 - 704 - 1999; 27 - 704 - 1999; 28 - 704 - 1999; 28 - 704 - 1999; 28 - 704 - 1999; 28 - 704 - 1999; 28 - 704 - 1999; 28 - 704 - 1999; 28 - 704 - 1999; 28 - 704 - 1999; 28 - 704 - 1999; 28 - 704 - 1999; 29 - 704 - 1999; 29 - 704 - 1999; 29 - 704 - 704 - 1999; 29 - 704 - 1999; 20 - 704 - 704 - 1999; 20 - 704 - 704 - 1999; 20 - 704 - 1999; 20 - 704 - 1999; 20 - 704 - 1999; 20 - 704 - 1999; 20 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 2099; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 704 - 1999; 21 - 
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16-AUG-1999;
17-AUG-1999;
18-AUG-1999;
20-AUG-1999;
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26-AUG-1999;
27-AUG-1999;
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23-AUG-1999
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Gaps
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               9905-0154039-9905-0154039-9905-0155139-9905-0155138-9905-0155486-9905-0155486-9905-0155486-9905-0155486-9905-0155486-9905-015528-9905-015923-9905-015923-9905-015923-9905-015923-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-015928-9905-0159
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Matches 14; Conservative
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22-071-1999;
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26-071-1999;
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28-071-1999;
28-071-1999;
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AAG38576 standard; Protein; 518 AA AAG38576; AAG38576

18-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 47611.

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thaliana

EP1033405-A2

06-SEP-2000.

25-FEB-2000; 2000EP-0301439

990S-0142977. 990S-0143542. 990S-0144005. 990S-0144005. 990S-01440065. 990S-01440085. 990S-0144333. 990S-0144333. 990S-0144334. 990S-0144334. 990S-0144334. 990S-0144338. 990S-0146338. 990S-0146338. 990S-0146338. 990S-0145218. 990S-0145218. 990S-0145913. 990S-0147302. 990S-0147302. 990S-0147302. 990S-0147303. 990S-0147303. 990S-0147303. 990S-0147303. 990S-0147303. 990S-0147303. 990S-0147303. 990S-0147303.	
12 - Jul 1999; 13 - Jul 1999; 14 - Jul 1999; 16 - Jul 1999; 17 - Jul 1999; 18 - Jul 1999; 19 - Jul 1999; 19 - Jul 1999; 19 - Jul 1999; 20 - Jul 1999; 21 - Jul 1999; 22 - Jul 1999; 23 - Jul 1999; 24 - Jul 1999; 25 - Jul 1999; 26 - Jul 1999; 27 - Jul 1999; 28 - Jul 1999; 28 - Jul 1999; 29 - Jul 1999; 20 - Jul 1999; 21 - Jul 1999; 22 - Jul 1999; 23 - Jul 1999; 24 - Jul 1999; 25 - Jul 1999; 26 - Jul 1999; 27 - Jul 1999; 28 - Jul 1999; 29 - Jul 1999; 20 - Jul 1999; 21 - Jul 1999; 22 - Jul 1999; 23 - Jul 1999; 24 - Jul 1999; 25 - Jul 1999; 26 - Jul 1999; 27 - Jul 1999; 28 - Jul 1999; 29 - Jul 1999; 20 - Jul 1999; 21 - Jul 1999; 22 - Jul 1999; 23 - Jul 1999; 24 - Jul 1999; 25 - Jul 1999; 26 - Jul 1999; 27 - Jul 1999; 28 - Jul 1999; 29 - Jul 1999; 20 - Jul 1999; 21 - Jul 1999; 22 - Jul 1999; 23 - Jul 1999; 24 - Jul 1999; 25 - Jul 1999; 27 - Jul 1999; 27 - Jul 1999; 28 - Jul 1999; 29 - Jul 1999; 20 - Jul 1999; 21 - Jul 1999; 22 - Jul 1999; 23 - Jul 1999; 24 - Jul 1999; 25 - Jul 1999; 26 - Jul 1999; 27 - Jul 1999; 27 - Jul 1999; 28 - Jul 1999; 29 - Jul 1999; 20 - Jul 1999; 21 - Jul 1999; 22 - Jul 1999; 23 - Jul 1999; 24 - Jul 1999; 25 - Jul 1999; 26 - Jul 1999; 27 - Jul 1999; 28 - Jul 1999; 29 - Jul 1999; 20 - Jul 1999; 21 - Jul 1999; 22 - Jul 1999; 23 - Jul 1999; 24 - Jul 1999; 25 - Jul 1999; 26 - Jul 1999; 27 - Jul 1999; 28 - Jul 1999; 29 - Jul 1999; 20 - Jul 1999; 20 - Jul 1999; 21 - Jul 1999; 22 - Jul 1999; 23 - Jul 1999; 24 - Jul 1999; 25 - Jul 1999; 26 - Jul 1999; 27 - Jul 1999; 28 - Jul 1999; 29 - Jul 1999; 20 - Jul 1999; 20 - Jul 1999; 21 - Jul 1999; 22 - Jul 1999; 23 - Jul 1999; 24 - Jul 1	27 - AUG-1999; 30 - AUG-1999; 31 - AUG-1999; 01 - SEP-1999; 07 - SEP-1999; 13 - SEP-1999; 13 - SEP-1999; 16 - SEP-1999; 20 - SEP-1999; 21 - SEP-1999; 22 - SEP-1999; 23 - SEP-1999; 24 - SEP-1999; 28 - SEP-1999;
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990S - 0121825 990S - 0121825 990S - 0123180 990S - 0126268 990S - 0126268 990S - 0126268 990S - 01262785 990S - 0128234 990S - 0130849 990S - 0130849 990S - 0131849 990S - 0131864 990S - 0132486 990S - 0134218 990S - 0134219 990S - 0134946 990S - 0139455 990S - 0139455 990S - 0139455 990S - 0139455 990S - 0139455 990S - 0139456 990S - 0139456 990S - 0139460 990S - 0139460	
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The present sequence is given in a specification relating to the structure and function of a regulatory gene, SCARECROW (SCR).

SCARECROW-like (SCL) genes encoding proteins containing an amino acid sequence similar to the sequence of MOTIF III (VHIID) of Arabidopsis SCR protein are disclosed. SCR and SCL genes are useful for producing it ransgenic plants whose cell division is modified and root and/or stem development and gravitropism of stem or hypocotyl is altered. Cell division is increased or decreased in roots resulting in thicker or thinner root development. The transgenic plants are useful for expressing a gene of interest encoding a gene product that confers herbicide, salt, pathogen or insect resistance in root or embryos and genes encoding starch, lignin or cellulose biosynthesis in shoots. The SCR gene also confers less assceptibility to lodging in the transgenic plants than a wild-type plant. SCR gene sequences are also useful as molecular markers for a quantitative trait e.g. root or gravitropism trait in molecular
                                           Scarecrow gene useful for producing transgenic plants expressing genes whose product increases starch, lignin or cellulose biosynthesis and confers herbicide, pathogen or insect resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana gibberellin insensitivty gai gene product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.4%: Score 70; DB 21; Length 531; 82.4%; Pred. No. 9.7e-05; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding gibberellin inhibitor GAI and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gibberellin insensitivity; gai; plant growth inhibition; dwarf phenotype; lodging resistance; increased yield; flowering regulation; bolting inhibition; spinach; lettuce; antibody; identification; probe; primer; antisense; sense; expression regulation; co-suppression; rice; Bakane disease resistance.
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                                                                                                              Claim 14; Fig 13; 200pp; English
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Matches 14; Conservative
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            WPI; 2000-594315/56.
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Pred. No. 9.5e-05;
2; Mismatches 1; Indels
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Helariutta Y, Bruce W, Lim J;
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99US-0158369,
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99US-0162142
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Best Local Similarity
Matches 14; Conserv
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                                                         07-OCT-1999;
08-OCT-1999;
12-OCT-1999;
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14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
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13-OCT-1999;
13-OCT-1999;
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14-0CT-1999;
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22-OCT-1999;
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26-0CT-1999;
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28-OCT-1999
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AAB28575
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                                                                            The present sequence is the Arabidopsis thaliana gibberellin insensitivity (gai) gene product (GAI), the expression of which inhibits plant growth. However the inhibition is antagonised by gibberellin (GA), while gai expression confers a dwarf phenotype gibberellin (GA), while gai expression confers a dwarf phenotype confere tall or dwarf plants, particularly the latter for increased resistance to lodging and increased yield. It may also allow resistance to lodging and increased yield. It may also allow regulation of flowering, i.e. plants remain in the vegetative state until treated with GA, useful to inhibit bolting in spinach and letture. GAI can be used to raise specific antibodies for identifying homologous proteins or genes in other species. gai fragments can also be used as probes or primers to identify and clone related sequences, or in the preparation of antisense or sense expression regulating (co-suppressing) sequences. Rice plants that express GAI may be resistant to Bakane disease. Manipulation of gai and GAI makes it possible to tallor the degree of dwarfism and GAI makes it possible to tallor the degree of dwarfism
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antisense sequences - used to create tall, or particularly, dwarf plants, especially crops such as maize, rice and wheat
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Pred. No. 9.7e-05;
Mismatches 1; Indels
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/note= "Conserved domain"
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270..274
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                                                Claim 1; Fig 4; 76pp; English
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82.4%;
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22-AUG-2000; 2000US-0227439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-2001 (first entry)
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Best Local Similarity 82.4
Matches 14; Conservative
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PILGRIM M.
ADAM L.
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HEARD J.
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The patent relates to polynucleotides encoding 35 plant transcription factors which may be used to modify phenotype associated with a plant's sugar sensing characteristics and increasing yield when their expression level is altered. Sugars are central regulatory molecules that control aspects of physiology, metabolism and development. Therefore the CDNAs and proteins of the invention are useful for modifying the growth and germination rates of plants, photosynthesis, glyoxylate metabolism, response, wounding response, cell cycle regulation, pigmentation, flowering and sensecence of plants and for modifying sink source relationships in seeds, tubers, roots, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and physical storage to alter the structure and developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. The present sequence is an Arabidopsis thaliana transcription factor.
                                                                                                                                                                             Nucleic acids encoding plant transcription factor polypeptides, useful for altering the sugar sensing characteristics of plants and increasing yield, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, onlon, papaya, peas, peppers, pineapple, spinach, squash, sweet corn,
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                                                                       Riechmann JL;
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                                                                       Pineda O, Pilgrim M, Adam L,
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Pred. No. 9.7e-05;
2; Mismatches 1;
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270..274
/label- Conserved_domain
                                                                                                                                                                                                                                                          Claim 4; Page 74-76; 151pp; English.
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Best Local Similarity 82.4
Matches 14; Conservative
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(RIEC/) RIECHMANN J L.
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                                                                       Heard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 AA;
                                  (SAMA/) SAMAHA R.
                                                                                                                                                N-PSDB; AAD06646
                                                                                          Samaha R;
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                                                                     Jiang C,
Yu G, Sar
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990S-0134768.
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990S-0135353.
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                                                                              2000EP-0301439
                 EP1033405-A2.
                                                                              25-FEB-2000;
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30-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is Arabidopsis thaliana transcription factor, (300, a homologue of G307. The transcription factor is used for altering a plant's biochemical characteristics. The transcription factor may be used to alter the structure and developmental characteristics of plants such as soybean wheat, corn, potato, cotton, rice, oilseed rape, such as soybean, wheat, corn, totato, cotton, rice, oilseed rape, sunfalfa, sugar cane, turf, banana, blackberry, blueberry, pubeberry, prapperry, cartaloupe, carrot, canliflower, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, pepplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, pepplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, pepplant, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. Transcription factors are key controlling elements of blological pathways and altering childpoiled pathways in an organism. Therefore manipulating transcription factor levels in plants offers great potential in agricultural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding plant transcription factor polypeptides, useful for altering the biochemical characteristics of plants e.g. corn, potato and cotton plants -
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                                                                                                                                                                                                                                                                       Samaha R;
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82.4%; Pred. No. 9.7e-05;
Live 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                       Adam L, Riechmann JL, Heard J,
), Jiang C;
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 114-115; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG38575 standard; Protein; 533 AA.
                                                                                           MENDEL BIOTECHNOLOGY INC.
                             17-NOV-1999; 99US-0166228.
17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
14-NOV-2000; 2000WO-US31344
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                         ADAM L.
RIECHMANN J L.
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Pilgrim M, Pineda O,
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N-PSDB; AAD05791.
                                                                                                           CREELMAN R.
                                                                                                                                                                      HEARD J.
SAMAHA R.
PILGRIM M.
PINEDA O.
JIANG C.
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                                                                                                                                                                                        (SAMA/)
(PILG/)
(PINE/)
(JIAN/)
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RR 01-JUL-1999; 99US-0141842.

RR 01-JUL-1999; 99US-0141842.

RR 01-JUL-1999; 99US-0141842.

RR 06-JUL-1999; 99US-014205.

RR 11-JUL-1999; 99US-014203.

RR 11-JUL-1999; 99US-01429.

RR 11-JUL-1999; 99US-014342.

RR 11-JUL-1999; 99US-014433.

RR 21-JUL-1999; 99US-014508.

RR 21-JUL-1999; 99US-014709.

RR 2
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Scarecrow gene; SCR gene; plant; regulatory gene; SCARECROW-like; SCL; transgenic plant; cell division; molecular marker; herbicide resistance; salt resistance; pathogen resistance; insect resistance.
                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                86.4%; Score 70; DB 21; Length 533;
82.4%; Pred, No. 9.8e-05;
ive 2; Mismatches 1; Indels
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9905 - 0154039
9905 - 0154039
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                                                                                                                                                                                                                                                                                                14; Conservative
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                                                                                                                                                                                                                                                                       Similarity
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14-SEP-2000
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Matches
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Pysh L;

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The present sequence is given in a specification relating to the structure and function of a regulatory gene, SCARECROW (SCR).

SCARECROW-like (SCL) genes encoding proteins containing an amino acid sequence similar to the sequence of MOTIF III (VHIID) of Arabidopsis SCR protein are disclosed. SCR and SCL genes are useful for producing transgenic plants whose cell division is modified and root and/or stem development and gravitropism of stem or hypocotyl is altered. Cell division is increased or decreased in roots resulting in thicker or thinner root development. The transgenic plants are useful for expressing a gene of interest encoding a gene product that confers herbicide, salt, pathogen or insect resistence in root or embryos and genes encoding starch, lighth or cellulose biosynthesis in shoots. The SCR gene also confers less susceptibility to lodging in the transgenic plants than a wild-type plant. SCR gene sequences are also useful as molecular markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scarecrow gene useful for producing transgenic plants expressing genes whose product increases starch, lignin or cellulose biosynthesis and confers herbicide, pathogen or insect resistance
                                                                                                                                                                                                                Di Laurenzio L, Wysocka-Diller J, Malamy JE, Y, Bruce W, Lim J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Fig 13; 200pp; English.
99US-0265585
                                                                                                     (UYNY ) UNIV NEW YORK STATE
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                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-594315/56.
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10-MAR-1999;
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587 AA;

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 Score 70; DB 21; Length 587; Pred. No. 0.00011;
                                    2; Mismatches
Query Match 86.4
Best Local Similarity 82.4
Matches 14; Conservative
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1 DELLAALGYKVRASDMA 17 g δλ

AAE02560 standard; Protein; 587 AA. RESULT

(first entry) 10-AUG-2001

AAE02560;

A. thaliana transcription factor G308 homolog, G307.

Plant transcription factor; phenotype; sugar sensing characteristic; transgenic plant; plant yield; growth; germinathon; photosynthesis; glyoxylate metabolism; respiration; pathogen response; wounding response; cell cycle regulation; pigmentation; flowering; senescence; physiology; storage organ; metabolism

Arabidopsis thaliana.

Location/Qualifiers 323..339 /note= "Conserved domain"

Domain

WO200135725-A1

25-MAY-2001.

14-NOV-2000; 2000WO-US31414

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The patent relates to polynucleotides encoding 35 plant transcription factors which may be used to modify phenotype associated with a plant's sugar sensing characteristics and increasing yield when their expression level is altered. Sugars are central regulatory molecules that control aspects of physiology, metabolism and development. Therefore the cobnast and proteins of the invention are useful for modifying the growth and germination rates of plants, photosynthesis, glyoxylate metabolism, respiration, starch and sucrose synthesis and degradation, pathogen response, wounding response, cell cycle regulation, pigmentation, flowering and senescence of plants and for modifying sink-source relationships in seeds, tubers, roots, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and polypeptides may be used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed, sunflower, alfalfa, sugarcane, tuff, banana, blackberry, colfee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, the papar, peas, peppers, pinapple, spinach, squash, sweet corn, confee, cucumber, eggplant, grape, honey dew, lettuce, mango, melon, the papar, peas, peppers, pensely plants, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding plant transcription factor polypeptides, useful for altering the sugar sensing characteristics of plants and increasing yield, e.g. corn, potato and cotton plants -
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Samaha R;
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Pred. No. 0.00011;
2; Mismatches 1;
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                                                                                                                                                                   MENDEL BIOTECHNOLOGY INC
                                   2000US-0197899.
2000US-0227439.
99US-0166228
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N-PSDB; AAD06661.
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HEARD J.
PINEDA O.
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22-AUG-2000;
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GenCore version 4.5
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OM protein – protein search, using sw model

(without alignments)
100.697 Million cell updates/sec ; Search time 12.86 Seconds December 19, 2001, 17:05:49 Run on:

US-09-485-529-104 81 1 DELLAALGYKVRASDMA 17 Perfect score: Sequence: Title:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		40					
Result	, ,	Query	4		f	•	
NO.	score	March	rengru	9	1D		Description
1	7.0	86.4	511	7	696688		hypothetical prote
7	70	86.4	523	~	T51475		RGA-like protein -
3	70	86.4	533	7	H86282		protein F10B6.34 [
4	7.0	Q	587	7	D84426		hypothetical prote
'n	46	56.8	495	~	C71679	_	UDP-n-acetylmurama
9	45	55.6	257	~	T10758	1	mandelonitrile lya
7	44	54.3	466	~	B69610		carboxy-terminal p
8	43	53.1	640	~	E64116		Ψ
σ	42	51.9	263	7	T01149		probable acetone-c
10	42	51.9	516	7	E96839		hypothetical prote
11	41		272	~	C72498		probable stress pr
12	41		311	~	A75047		2-ketovalerate oxi
13	41	50.6	314	7	B71114		probable ferredoxi
14	41		454	7	B70418		UDP-N-acetylmurama
15	41		463	7	D81960		ATP-dependent DNA
16	41		469	7	B81201		UDP-N-acetylmurama
17	41	20.6	484	~	C84955		UDP-N-acetylmurama
18	41	-	491	- 	CEECAM		UDP-N-acetylmurama
19	41		491	7	G85491		hypothetical prote
20	41	50.6	206	7	A81777		UDP-N-acetylmurama
21	41	50.6	550	~	T37519		probable amino aci
22	41	50.6	1002	~	S70292		FUN12 protein - ye
23	40	49.4	96	~	083600		Q.
. 24	40	49.4	330	7	A83417		probable oxidoredu
25	40	49.4	477	7	E82763		UDP-N-acetylmurama
26	40		480	7	D83094		UDP-N-acetylmurama
27	40	49.4	700	~	T49445		adrenoleukodystrop
28	40	49.4	957	7	T10633		
29	39	48.1	82	7	A72274		hypothetical prote

conserved hypothet probable (S)-aceto	probable ribosomal hypothetical prote	probable acetone-c 2,2',3-trihydroxyb	probable molybdenu	spermidine/putresc	spermidine/putresc hypothetical prote	spermidine/putresc probable UDP-N-ace	hypothetical prote cholecystokinin ty
H75570 T02428	A71186 S76919 E83600	T01151 A49932	H81448	F82201 .	A40840 F85683	B64118 C71338	B84221 T19135
77	m # c	400	·~·	77	m m	22	3.45
136	188	262	537	37.	378	38,	64
48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1 48.1
39	5 6 6 6 6 6	0 0 0 0 0	38	200	9 9 9	6 6 8 6 8 6	3 3 3 8
30	3 3 3 3 3 3 3	# IA 90 5 m m	37	8 6 F	40	42 43	44 45

ALIGNMENTS

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Dypothetical protein T27F4.10 [imported] - Arabidopsis thaliana chypothetical protein T27F4.10 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G96688
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, R.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzoberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Thle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; Muid:21016719
A;Accession: G96688
A;Status: preliminary
A;Molecule turner

A;Molecule rype: DNA A;Residues: 1-511 <STO> A;Cross-references: GB:AE005173; NID:g10092507; PIDN:AAG12907.1; GSPDB:GN00141 C;Genetics:

A;Gene: T27F4.10 A;Map position: 1

ö Gaps ; 0 Length 511; Score 70; DB 2; Length 511 Pred. No. 0.00017; 1; Mismatches 2; Indels 86.4%; 82.4%; Ouery Match 86.4 Best Local Similarity 82.4 Matches 14; Conservative

1 DELLAALGYKVRASDMA 17 ò

32 DELLVVLGYKVRSSDMA 48 g

~ RESULT

RGA-like protein - Arabidopsis thaliana
N;Alternate names: protein K3M16_60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: T51475
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; submitted to the Protein Sequence Database, August 2000

A; Reference number: Z25394 A; Accession: T51475 A; Status: preliminary

A,Molecule, type: DNA,
A,Residues: 1-523 <SAT>
A,Cross-references: EMBL:AL391150
A,Experimental source: cultivar Columbia; BAC clone K3M16

a

protein F10B6.34 (imported) - Arabidopsis thaliana

RESULT H86282

86.4%;

Query Match 86.4 Best Local Similarity 82.4 Matches 14; Conservative

A; Map position: 3 A; Note: K3M16_60

C; Genetics:

8

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1 DELLAALGYKVRASDMA 17

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N'Alternate names: hydroxynitrile lyase
C;Species: Hevea brasiliensis (Para rubber tree)
C;Accession: 10758
C;Accession: 110758
R;Hasslacher, M.; Schall, M.; Hayn, M.; Griengl, H.; Kohlwein, S.D.; Schwab, H.
J. Biol. Chem. 271, 5884-5891, 1996
A;Title: Molecular-cloning of the full-length cdna of (s)-hydroxynitrile lyase from h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Date: 21. Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C; Accession: C71679
R; Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark Nature 396, 133-140, 1998
A; Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A; Reference number: A71630; MUID:99039499
A; Stetus: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: catalyzes the conversion of mandelonitrile to benzaldehyde and cyanide A; Note: involved in the biodegradation of cyanogenic glycosides; also catalyzes the s C; Keywords: aldehyde-lyase; carbon-carbon lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14709.1; PID:g386
A;Experimental source: strain Madrid E
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A;Molecule type: mRNA
A;Residucs: 1-257 <HRA>
A;Residucs: 1-257 <HRA>
A;Cross-references: EMBL:U40402; NID:g1223883; PIDN:AAC49184.1; PID:g1223884
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  UDP-n-acetylmuramate--alanine ligase (murC) RP247 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Pred. No. 3.1;
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                                          Indels
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Pred. No. 0.00019;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.6%; Score 45; DB 2; 66.7%; Pred. No. 2.4; 11ve 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: UDP-N-acetylmuramate--alanine ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
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A; Accession: T10758
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60.0%;
    82.48;
                                                                                                                            1 DELLAALGYKVRASDMA 17
                                                                                                                                                                           44 DELLAVLGYKVRSSEMA 60
                                          14; Conservative
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:| |||||:| ||:
31 EILHNLGYKVQGSDL 45
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Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-495 <AND>
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A;Gene: murC; RP247
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Matches 1
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C;Date: 02-Mar-2001 sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H86282
R;Theologis, A.; Ecker, J.R.; Falm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Mature 408, 816-820, 2000
R;Authors: Hulzar, L.
Ratzo, M.; Rooney, T.; Rowley, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
R, Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Ratzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M.
Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M.
Rytitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
Rythere on umber: A66141; MUID:21016719
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                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                             Length 523;
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                                                                                                                                                                                                         Score 70; DB 2; Length 523
Pred. No. 0.00017;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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Score 70; DB 2; I Pred. No. 0.00018; 2; Mismatches 1;

86.48;

Query Match 86.4 Best Local Similarity 82.4 Matches 14; Conservative

Residues: 1-533 <STO> Status: preliminary Molecule type: DNA

A; Map position: 1

A; Gene: F10B6.34

C; Genetics:

g

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86.4%; Score 70; DB 2;

Residues: 1-587 <STO>

A,Gene: At2g01570 A,Map position: 2

C; Genetics:

Query Match

Status: preliminary Molecule type: DNA

Length 587;

Gaps

ö

Indels

Length 640;

5,

C; Superfamily: exodeoxyribonuclease V 67K chain

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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hudhes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A; Authors: Hunter, J.L.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                      N.Alternate names: hypothetical protein F2686.25
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C;Accession: T01149; G84626
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F2686 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-263 <ROU>
A;Resoretereness: BMBL:AC003040; NID:g3242700; PID:g3242721
A;Cross-references: EMBL:AC003040; NID:g3242700; PID:g3242721
A;Experimental source: cultivar Columbia
B;Lin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: G84626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: AE002093; NID: 93242721; PIDN: AAC23773.1; GSPDB: GN00139
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                   probable acetone-cyanohydrin lyase [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F23A5.6 [imported] - Arabidopsis thaliana
                                          ore 43; DB ed. No. 14; Mismatches
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3; Mismatches
                                             Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: translated from GB/EMBL/DDBJ
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60.0%;
                                          53.1%;
69.2%;
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Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                       Conservative
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LLEALGHRVTALDLA 43
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                                                                                                                                                                                                                    355 LLATTGYKVEGSD 367
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                                                                                                                                                              3 LLAALGYKVRASD 15
                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Status: preliminary
A Molecule type: DNA
A; Residues: 1-263 <STO>
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A;Cross-references: GB:299114; GB:AL009126; NID:g2634230; PIDN:CAB13850.1; PID:g2634351 A;Experimental source: strain 168 R;Marasco, R.; Varcamonti, M.; Ricca, E.; Sacco, M. Gene 183, 149-152, 1996 A;Title: A new Bacillus subtilis gene with homology to Escherichia coli prc. A;Reference number: JC5744; MUID:97149292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-297, 'RSRNYGRC', 306-466 <MAR>
A; Cross-references: EMBL:X98341; NID:g1402943; PIDN:CAA66987.1; PID:g1402944
A; Experimental source: strain PY17
C; Comment: This protein is presumed to be involved in cleavage of the carboxyl-terminal
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630
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C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 2; Length 466;
Pred. No. 6.6;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: carboxyl-terminal processing proteinase C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.3%;
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Best Local Similarity 53.3
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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A;Start codon: TTG
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Length 263;

DB 2;

8.4;

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probable ferredoxin oxidoreductase beta subunit - Pyrococcus horikoshii
C;Species: Diagraps #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: B71114
R;Kawarabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
M; Ohiuku, Y; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili
A;Reference number: A71000; MUID:98344137
A;Reference number: A71000; MUID:98344137
A;Status: preliminary: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Status: 1-314 «KAMA»
A;Ressidues: 1-314 «KAMA»
A;Cross-references: GB:AP000003; NID:93236130; PIDN:BAA29772.1; PID:93257089
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBa
C;Genetics:
A;Gene: PH0681
C;Superfamily: pyruvate synthase beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B70418
UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8) - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Jul-1999
C;Accession: B70418
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE000736; NID:g2983763; PIDN:AAC07323.1; PID:g2983764; GB:AE00
A;Experimental source: strain VF5
C;Genetics:
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A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A; Reference number: A70300; MUID:98196666
A; Accession: B70418
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-454 < AQF>
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Pred. No. 15;
1; Mismatches
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Pred. No. 22;
5; Mismatches
  Pred. No. 15;
1; Mismatches
  66.78;
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Best Local Similarity 43.8
Matches 7; Conservative
  Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                               90 LKALGYKVKGED 101
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Best Local Similarity
Matches 8; Conserv
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C; Superfamily
C; Keywords: 1:
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999
B; R;Rawarabayasi, Y.; Hano, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kona, Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339
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A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru A; Reference number: A75001
A; Recession: A75047
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A;Molecule type: DNA
A;Residues: 1-272 <KRM>
A;Cross-references: DDBJ:AP000063; NID:95105654; PIDN:BAA80971.1; PID:95105659
                                               A;Molecule type: DNA
A;Residues: 1-516 <STO>
A;Cross-references: GB:AE005173; NID:g6503282; PIDN:AAF14658.1; GSPDB:GN00141
C;Genetics:
A;Gene: F23A5.6
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C72498
probable stress protein APE1961 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                 4; Indels
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Pred. No. 13;
7; Mismatches
                                                                                                                                                                                                                                                         DB 17;
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                                                                                                                                                                                                                                                            Score 42;
Pred. No.
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C,Superfamily: aldehyde reductase
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A; Accession: E96839
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Genetics:

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C: Detectors: Netscaria meningitidis (strain 22491 ser C: Species: Netsseria meningitidis (strain 22491 ser C: Species: Netsseria meningitidis
C: Species: Netsseria meningitidis
C: Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C: Accession: D81960
R: Parkhill, J: Achtman, M: James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A: Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A: Accession: D81960
A: Accession: D81960
A: Accession: D81960
A: Status: preliminary
A: Molecule type: DNA
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A: Residues: 1-463 < PAR>
A: Cross-references: GB:AL157959; NID:q7379120; PIDN:CAB83732.1; PID:q737918
A: Experimental source: serogroup A, strain 22491
C: Genetics:
A: Genetics:
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Search completed: December 19, 2001, 17:07:48 Job time: 119 sec

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Score 41; DB 2; Length 463; Pred. No. 22; 4; Mismatches 2; Indels

Ouery Match 50.6%; Best Local Similarity 57.1%; Matches 8; Conservative

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Compugen Ltd
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GenCore version
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EX5A_HAEIN
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P28595 P34913 P3491329 P43329 P60109 P96848 Q57989 Q14055 P4566	ENTS 495 AA.	update) on update) ? (EC 6.3.2.8) (UDP-N-	ion; Rickettsiale	Andersson J.O., ., Podowski R.M., Naeslund and C.G.; prowazekii and the origin	THE STATEMENT OF THE PROBABLE FUNCTION (BY SIMILARITY). FUNCTION: CELL WALL FORMATION (BY SIMILARITY). CATALYTIC ACTIVITY: APP + UDP-N-ACETYLMURAMOYL + L-ALANINE ADP + ORTHOPHOSPHARE + UDP-N-ACETYLMURAMOYL-L-ALANINE. PATHWAY: PEPTIDGGLYCAN BIOSYNTHESIS. SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE). SIMILARITY: BELONGS TO THE MURCDEF FAMILY.	roduced thr ics and th re are no as its cont Usage by http://www.	EMBL; AJ235271; CAA14709.1; InterPro; IPR000713; Mur_ligase. Faffan; PF01225; Mur_ligase. Peptidoglycan synthesis; Cell wall; Cell division; Ligase. ATP-binding; Complete proteome. NP_BIND 120 126 ATP (POTENTIAL). SEQUENCE 495 AA; 54612 MW; 2E18464088FAD2D6 CRC64;	DB 1; Length 495 1.4; ches 3; Indels	
PYRG_AZOBR HYES_HUMAN IF2P_HALHA HRPA_ECOLI HRPA_HAEIN VG35_HSVII NAT_MYCTU HRM3_METJA METC_BORAV SYYC_SCHPO MURC_HAEIN IF2P_SULAC	ALIGNMENT PRT; 495	uence v otatior LIGASE ETASE)	alpha subdiv eae; Ricketts	<pre>Med=9823893; horodipour A., Andersson . Alsmark U.C.M., Podowski ler H.H., Kurland C.G.; of Rickettsia prowazekii</pre>	ORMATION (BY TP + UDP-N-AC+ + UDP-N-ACETY N BIOSYNTHESI CYTOPLASMIC	copyright. It ute of Bloinf cs Institute. itutions as lint is not remise agreement see@isb-sib.ch	09.1; ur_ligase. lase; 1. s; Cell wall; Ce proteome. ATP (POTE	8; Score 46; DB 8; Pred. No. 1.4 3; Mismatches	
45.7 544 45.7 583 45.7 1300 45.7 1300 45.7 1304 44.4 283 44.4 283 44.4 401 44.4 401 44.4 401	STANDARD;	USZUSSA 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last seq 20-AUG-2001 (Rel. 40, Last ann UDP-N-ACETYLMURAMATEALANINE ACETYLMURAMOYL-L-ALANINE SYNTH MURC OR RP247, Rickettsia prowazekii.		STRAIN-MADRID E; MEDLINE-90139499; PUDMed-9823893; Andersson S.G.E., Zomorodipour A., Sicheritz-Ponten T., Alsmark U.C.M Eriksson AS., Winkler H.H., Kurli "The genome sequence of Rickettsla	33-140(1998). CELL WALL F. CACTIVITY: R. THOPHOSPHATE PEPTIDOGINCA TAR LOCATION: TY: BELONGS I	This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are noise by non-profit institutions as long as its modified and this statement is not removed. Usage entities requires a license agreement (See http://or send an email to license@isp-sib.ch).	271; CAA14709 1; PR000713; Mur_liga PR000713; Mur_ligas; 1. an synthesis; Coll COMplete proteom 120 126 495 AA; 54612 MW;	tch 56.8%, al Similarity 60.08, 9; Conservative ELLAALGYKVRASDM 16	
334 335 335 337 337 338 337 337 340 340 341 341 344 344 344 344 345 346 344 346 346 346 346 346 346 346 346	RESULT 1 MURC_RICPR ID MURC_RICPR	UYZDS8; 30-MAY-2000 (30-MAY-2000 (20-AUG-2001 (UDP-N-ACETYLM AURC OR MYRC OR MYRC OR MYRC OR MYRC OR MYRC OR MYRC OF MYRC OR MYRC OF MYRC OR MYRC OR MYRC OF MYRC O	Bacteria; Prot Rickettsiaceae NCBI_TaxID=782 [1] SEQUENCE FROM	STRAIN-MADRID MEDLINE-990394 Andersson S.G Sicheritz-Pont Eriksson AS. "The genome se	Nature 396:10 Nature 396:10 -1- CATALYTI ADP + OR -1- PATHWAY: -1- SUBCELLU	This SWISS-I between the the European use by non modified and entities reg	EMBL; AJ35577 EMBL; AJ35577 Pram; PF01225, Peptidoglycan APP-binding; (NP_BIND 15) SEQUENCE 499	Query Match Best Local Simi Matches 9; 2 ELLAALG	
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Length 257; 3; Indels

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55.6%;

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Similarity

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SEQUENCE MUTAGEN

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EF4AE88717279CEB CRC64; S->A: LOSS OF ACTIVITY C->S: LOSS OF ACTIVITY H->A: LOSS OF ACTIVITY

207 235 235 80 81 235 257 AA;

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PDB; 6YAS; 13-OCT-99.
PDB; 1QJ4; 10-OCT-99.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000379; Est_11p_thioest_actsite.
Pfam; PF00561; abhydrolase; 1.

Lyase; 3D-structure.

us-09-485-529-104.rsp

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us2704;
11-OCT-1996 (Rel. 34, Created)
11-OCT-1996 (Rel. 34, Last sequence update)
130-MAY-2000 (Rel. 39, Last annotation update)
130-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Hevea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning of the full-length cDNA of (S)-hydroxynitrile lyase from Hevea brasiliensis. Functional expression in Escherichia coli and Saccharomyces cerevisiae and identification of an active site residue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

WEDLINEW-6434327, Pubmed-8805565;
Wagner U.G., Hasslacher M., Griengl H., Schwab H., Kratky C.;
Wechanism of cyanogenesis: the crystal structure of hydroxynitrile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.72 ANGSTROMS).

BUDLINE-20014021, Pubmed--10548044,

Zuegg J., Gruber K., Gugganig M., Wagner U.G., Kratky C.;

"Three-dimensional structures of enzyme-substrate complexes of the hydroxynitrile lyase from Hevea brasiliensis.";

Protein Sci. 8:1990-2000(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
MEDLINE-99423043; PubMed-10494852;
Gruber K., Gugganig M., Wagner U.G., Kratky C.;
"Atomic resolution crystal structure of hydroxynitrile lyase from Hevea brasiliensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96215058; Pubmed-8621461;
Hasslacher M., Schall M., Hayn M., Griengl H., Kohlwein S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: HOWODIMER.
-!- PTM: THE N-TERMINUS IS BLOCKED.
-!- SIMILARITY: DISTANT RELATIONSHIP WITH TYPE-B
CARBOXYLESTERASE/LIPASE FAMILY.
                                 257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                    Hevea brasiliensis (Para rubber tree).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 271:5884-5891(1996).
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyase from Hevea brasiliensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 380:993-1000(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Structure 4:811-822(1996).
                                     STANDARD;
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                                 HNL_HEVBR
P52704;
HNL_HEVBR
                                 DDBR BERREAR B
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=RD, KW20, ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Relacinann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McRenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: EXONUCLEOLYTIC CLEAVAGE (IN THE PRESENCE OF ATP) IN EITHER 5'-TO 3'-OR 3'-TO 5'-DIRECTION TO YIELD 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I-FUNCTION: EXHIBITS SYPERAL CATALYTIC ACTIVITIES, INCLUDING
ATP-DEPENDENT EXONUCLEASE, ATP-STIMULATED ENDONUCLEASE,
ATP-DEPENDENT UNMINDING AND DANA DEPENDENT ATPAGE ACTIVITIES.
STRAND CLEAVAGE OCCURS 5' TO 3' DURING THE UNMINDING OF DUPLEX
DNA AT CHI SEQUENCES, WHICH LOCALLY STIMULATE RECOMBINATION
(BY SIMILARITY).
                                                                                                                                                                                                                                      Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
EXODEOXYRIBONUCLEASE V ALPHA CHAIN (EC 3.1.11.5).
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                                                                                                            STANDARD;
25 LLEALGHKVTALDLA 39
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=727;
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                                                                                                       EX5A_HAEIN
P45158;
                                                                                      EX5A_HAEIN
                                                                RESULT
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EMBL; U40402; AAC49184.1; -.

1YAS; 16-JUN-97. 2YAS; 13-OCT-99. 3YAS; 13-OCT-99. 4YAS; 13-OCT-99. 5YAS; 13-OCT-99.

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FERREDOXIN OXIDOREDUCTASE BETA SUBUNIT)
             VORB OR PH0681
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067373;
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                                 Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
DNA repair; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                      'Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_raxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
KETOISOVALERATE OXIDOREDUCTASE SUBUNIT VORB (EC 1.....) (VOR) (2-OXOISOVALERATE OXIDOREDUCTASE BETA CHAIN) (2-OXOISOVALERATE-
                                                                                                                                                                                                                                                              20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
CONTOCALERATE OXIDOREDUCTASE SUBUNIT VORB (EC 1.....) (VOR) (2-CONTSCOVALERATE OXIDOREDUCTASE BETA CHAIN) (2-OXOISOVALERATE-FERREDOXIN OXIDOREDUCTASE BETA SUBUNIT).
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                                                                                                      53.1%; Score 43; DB 1; Length 640; 69.2%; Pred. No. 6.2;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
AA; 34759 MW; 1EBE2609519DAC30 CRC64;
                                                        TP (POTENTIAL).
C3C530AC398B5DA0 CRC64;
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                                                                                                                                                                                                                                  311 AA.
                                                                                                                            0; Mismatches
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                                                         ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAMMA CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
                                                                   640 AA; 72864 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ248287; CAB50270.1; -
U32811; AAC22967.1;
P09980; IUAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  structure and evolution."
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Best Local Similarity 66.7
                                                                                                                             Conservative
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                                                                                       Query Match
Best Local Similarity
'... 9; Conserve
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EMBL; U32811; AHSSP; P09980; ITIGR; HI1322;
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ORSAY;
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O58414;
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Q9UYZ2;
                                                                   SEQUENCE
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                                                        NP_BIND
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                                                                                                                                                                                                                             Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.; Masuchi Y., Shizuya H., Kikuchi H.; Thermophilic archaebacterium, Pyrococcus horikoshii OT3."; DNA Res. 5:55-76(1998).
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                 Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
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-1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
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-!- PATHWAX: PEPTIOGGLYCAN BIOSYWHESIS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UDP-N-ACETYIMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
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SEQUENCE 311 AA; 34569 MW; E27B65877EF65813 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.6%; Score 41; DB 1; 66.7%; Pred. No. 6.8:
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NCBI_TaxID=63363;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACETYLMURAMOYL-L-ALANINE SYNTHETASE)
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                                                                                                                                                                                                        MEDLINE-98344137; PubMed-9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAMMA CHAIN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
Pyrococcus horikoshii.
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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30-MAY-2000 (Rel.
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                                                                                                                                                                                                                                                                                                                Gaps
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MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                      EMBL; AE000736; AAC07323.1; -
InterPro; IPR000713; Mur_ligase.
Pfam; PF01225; Mur_ligase; 1.
Pptidoglycan synthesis; Cell wall; Cell division; Ligase;
ATP-binding; Complete proteome.
NP_BIND 113 119 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 454; Pred. No. 9.9;
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Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                             113 119 ATP (POTENTIAL).
454 AA; 50893 MW; 12665EE14448232C CRC64;
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484 AA; 54311 MW; 06359D435D5590A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 AA
                                                                                                                                                                                                                                                                                                              5; Mismatches
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InterPro; IPR001064; Crystallin.
InterPro; IPR000713; Mur_ligase.
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NP_BIND 125 131 AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                              50.6%;
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                            2 ELLAALGYKVRASDMA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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(Rel. 40,
(Rel. 40,
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SEQUENCE
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SEQUENCE
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MEDLINE=95324553; Pubmed=7601127;
Liger D., Masson A., Blanot D., van Heijenoort J., Parquet C.;
"Over-production, purification and properties of the uridine-diphosphate-N-acetylmuramate:L-alanine ligase from Escherichia coli.";
Eur. J. Blochem. 23.980-87(1995).
-!- FUNCTION: CELL WALL FORMATION.
-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE =
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ikeda M., Wachi M., Jung H.K., Ishino F., Matsuhashi M.; "Nucleotide sequence involving murG and murC in the mra gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MILLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
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Conditionally lethal Escherichia coli murein mutants contain point
defects that map to regions conserved among murein and folyl poly-
gamma-glutamate ligases: identification of a ligase superfamily.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.; Systematic sequencing of the Escherichia coli genome: analysis the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
                                                                                              ö
                                Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coll K-12."; Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                              MURC_ECOLI STANDARD; PRT; 491 AA.
17952; 007099;
01-NOV-1990 (Rel. 16, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-1991 (Rel. 40, Last annotation update)
UDP-N-ACETYLMURANATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-ACETYLMURANATE--ALANINE SYNTHETASE).
                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                             Score 41; DB 1;
Pred. No. 11;
                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 18:4014-4014(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (MUTANT MURC3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CGSC 5988;
MEDLINE-97309380; Pubmed-9166795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90326550; PubMed=2197603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92334977; PubMed=1630901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 36:6223-6229(1997).
                                                                                              'n
                      50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region of Escherichia coli.";
                                                                                                  Conservative
                                                                                                                                                             3 LLAALGYKVRASDM 16
                                                                                                                                                                                                                       37 ILLKLGYKVSGSDL 50
Query Match
Best Local Similarity
'... 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MURC OR B0091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia
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Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTECRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                               EMBL; X52644; CAA36868.1; --
EMBL; X5034; CAA38868.1; --
EMBL; D10483; BAA01356.1; --
EMBL; D600118; AAC73202.1; --
EMBL; U67892; AAB60787.1; --
PIR; J00545; CEECAM.
PIR; 340601; S40601.
Eccedenc; EG10619; murC.
InterPro; DR000713; Mur_ligase.
Pfam; PF01225; Mur_ligase; 1.
Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 G->D: IN MURC3.
53626 MW; D201B35931C013FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE AMINO-ACID PERMEASE C11D3.08C.
SPACILD3.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    550 AA
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002293; AA_rel_permease_1.
InterPro; IPR002027; Amino_acid_permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.6%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ELLAALGYKVRASDMA 17
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37 EVLANEGYQISGSDLA 52
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Best Local Similarity
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Q10087;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- FUNCTION: FUNCTION IN GENERAL TRANSLATION INITIATION BY PROMOTING THE BINDING OF THE FORMYLMETHIONINE-TRNA TO RIBOSOMES. SEEMS TO
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=S288C / AB972;
MEDLINE=95249563; PubMed=7731988;
Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sutrave P., Shafer B.K., Strathern J.N., Hughes S.H.; "Isolation, identification and characterization of the FUN12 gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi S.K., Lee J.H., Zoll W.L., Merrick W.C., Dever T.E., "Promotion of met-tRNAiMet binding to ribosomes by yIF2, a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'The nucleotide sequence of chromosome I from Saccharomyces
                                                                                                                                                                            Length 550;
                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                     POTENTIAL.
3DD1EF6003896E4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995)
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                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
TRANSLATION INITIATION FACTOR IF-2.
                                                                                                                                                                          Score 41; DB 1
Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                   PRT; 1002 AA
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                    POTENTIAL.
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MEDLINE-94357438; PubMed-8076820;
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201 221 246 266 93 356 406 406 431 473 E 501 PC. 59918 MW;
                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IF2 homolog in yeast.";
Science 280:1757-1760(1998).
                                                                                                                                                                          50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae.";
Gene 146:209-213(1994).
                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-S288C / AB972;
                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                  1 DELLAALGYK 10
                                                                                                                                                                                                                                                           32 DELLMSLGYK 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Storms R.K.;
                                                                                                                                                                                                                                                                                                                                IF2P_YEAST
P39730;
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TRANSMEM
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IF2P_YEAST
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94 LLAAVDYKLKAS 105
              3 LLAALGYKVRAS 14
                                                                                                                                                                                                                       Sphingomonas.
NCBI_TaxID=13689;
                                                                                                                                                                                                                                                                                                                                                                                        Armengaud J.;
                                                                                                                  P47243;
01-FEB-1996
                                                                                                       DBFB_PSEPA
                                                                                                                                                                                                                                                                         STRAIN=RW1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAMILY
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                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profil institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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 entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosuqi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBL_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                        Score 41; DB 1; Length 1002; Pred. No. 22; 4; Mismatches 3; Indels
                                                                                                                                                      GTP (BY SIMILARITY).
W; 1A496195DAE1C283 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probon; PD001076; Ribosomal_L5; 1.
PR05TTE; PS00358; RIBOSOMAL_L5; FALSE_NEG.
Ribosomal protein; Complete proteome.
SEQUENCE 188 AA; 21610 MW; 56CAP0B5053AECF4 CRC64;
                                                                                                                              Initiation factor; Protein biosynthesis; GTP-binding.
DOMAIN 361 371
                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SOS RIBOSOMAL PROTEIN LSP.
                                                                                                                                                                                                                                                                                                                                                 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
             or send an email to license@isb-sib.ch)
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Pfam; PF00281; Ribosomal_L5; 1.
Pfam; PF00673; Ribosomal_L5_C; 1.
                                   EMBL; U12980; AAC04996.1; -.
EMBL; L29389; AAA57228.1; ALT_SEQ.
EGD; SG0000033; FUNI2.
INTERPRO; IPR000795; GTP_EFTU.
INTERPRO; IPR000178; IF2.
                                                                                                                                                    412 419 GTF
1002 AA; 112268 MW;
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                                                                                                                                                                                                          50.6%;
                                                                                       Interpro; IPR000178; IF2.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF02131; IF2; 1.
                                                                                                                                                                                                                                   Conservative
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698 EVKAALGVKIAANDL 712
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                           ELLAALGYKVRASDM 16
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus horikoshii
                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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ID RL5_PYRHO
AC 059431;
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SEQUENCE
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-!- FUNCTION: RESPONSIBLE FOR META CLEAVAGE OF THE FIRST AROMATIC RING OF 2,2,3-TRIHYDROXYBIPHENYL. 2,2,3-TRIHYDROXYDIPHENYL. 2,2,3-TRIHYDROXYDIPHENYL. 2,2,3-TRIHYDROXYDIPHENYL. ETERS, CATECHOL, 3-METHYLCATECHOL, AND 4-METHYLCATECHOL ARE OXIDIZED LESS EFFICIENTLY AND 3,4-DIHYDROXYBIPHENYL. IS OXIDIZED CONSIDERABLY LESS EFFICIENTLY.
-!- COFACTOR: FERROUS ION:
-!- PATHWAY: KEY ENZYME IN THE DEGRADATION PATHWAYS OF DIBENZO-P-DIOXIN AND DIBENZOFURAN (SECOND STEP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Happe B., Eltis L.D., Poth H., Hedderich R., Timmis K.N.; "Characterization of 2,2", 3-trihydroxybiphenyl dioxygenase, an extradiol dioxygenase from the dibenzofuran- and dibenzo-p-dioxin-degrading bacterium Sphingomonas sp. strain RWI."; J. Bacteriol. 175:7313-7320(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas paucimobilis (Sphingomonas paucimobilis).
Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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NON (BY SIMILARITY).
E77B673329C87B32 CRC64;
                                                                                                                01-FEB-1996 (Rel. 33, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
2,2',3-TRIHYDROXYBIPHENYL DIOXYGENASE (EC 1.13.11.-).
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293 AA.
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PROSITE; PS00082; EXTRADIOL_DIOXYGENAS; 1
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InterPro; IPR000325; Glyoxalase_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 1-63
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PRT;
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STANDARD;
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Matches 8; Conserva
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208
259
293 AA;
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Gaps

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1; Indels

3; Mismatches

Best Local Similarity 66.7 Matches 8; Conservative

Query Match

48.1%; Score 39; DB 1; Length 188; 66.7%; Pred. No. 9.2;

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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Satto N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 127-28.0 min region on the linkage map.";
                          SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935, PubMed-11206551;

MEDLINE-21074935, PubMed-11206551;

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

"Genome sequence of enterchaagic Escherichia coli 0157:H7.";
                                                                                                                             "The complete genome sequence of Bscherichia coli K-12."; Science 277:1453-1474(1997).
J. Biol. Chem. 266:20928-20933(1991).
                                                                                                                                                                                     STRAIN-K12;
MEDLINE-97061202; PubMed-8905232;
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                  Gregor J., Davis
Mau B., Shao Y.;
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                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                            Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBL_TaxID=2261;
                                                                                                         30-MAY-2000 (Rel. 39, Last sequence update)
V-AAY-2000 (Rel. 39, Last annotation update)
KETOISOVALERATE OXIDOREDUCTASE SUBUNIT VORB (EC 1.....) (VOR) (2-OXISOVALERATE OXIDOREDUCTASE BETA CHAIN) (2-OXOISOVALERATE-
WORD OXIDOREDUCTASE BETA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Furuchi T., Kashiwagi K., Kobayashi H., Igarashi K.; "Characteristics of the gene for a spermidine and putrescine transport system that maps at 15 min on the Escherichia colichromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.1%; Score 39; DB 1; Length 311; 58.3%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA.
POTA OR B1126 OR Z1831 OR ECS1571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 AA; 34766 MW; 07CC02452E3C6074 CRC64;
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                                                                       311 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 1-7
                                                                       PRT;
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MEDLINE-96125254; PubMed-8550425;
                                                                                                30-MAY-2000 (Rel. 39, Created)
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Matches 7; Conservative
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                                                                       STANDARD;
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 61 LAAIGWNVDPSDLA 74
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90 LKAMGYKVKGED 101
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                                                                                                                                                                                                   Pyrococcus furiosus.
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                                                                      VORB PYRFU
Q51802;
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POTA_ECOLI
                                         RESULT 13
VORB_PYRFU
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                                                                                                       STRAIN—2157:H7 / RIMD 0509952;

X MEDLINE—21156231; PubMed=11258796;
A Hayashi T., Makinon K., Ohilshi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makinon K., Ohilshi M., Murata T., Tanaka M., Tobe T.,
A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
A Kuhara S., Shiba T., Hattori M., Shinagawa H.;
T. Complete genome sequence of enterchemorrhagic Escherichia coli
T. O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
C -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
FOR SPERMIDINE/PUTRESCINE. PROBABLY RESPONSIBLE FOR ENERGY
COUPLLING TO THE TRANSPORT SYSTEM.
C -!- SUBLIARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EcoGene; EG10749; pota.
InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; APP_GTP_A.
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Nature 409:529-533(2001).
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                                                                                 SEQUENCE FROM N.A.
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                                       PROSITE; PSO0211; ABC_TRANSPORTER; 1.

Transport; ATP-binding; Inner membrane; Complete proteome.

NP_BIND 50 57 ATP (BY SIMILARITY).

SEQUENCE 378 AA; 43028 MW; 14DCA99329A344F3 CRC64;
                                                                                                                                                                                                      Length 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA.
                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                    DB 1;
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 AA
                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                    Score 39;
Pred. No. 1
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InterPro; IPR003439; ABC_transportr.
InterPro; IPR001689; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.
SWART; SW00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                      48.18;
66.78;
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Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                              Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                          SMART; SM00382; AAA; 1.
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172 DESLSALDYKLR 183
                                                                                                                                                                                                                                                                                                      1 DELLAALGYKVR 12
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01-NOV-1995 (
20-AUG-2001 (
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P45171;
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POTA_HABIN
IDD POTA_HABIN
DT 01-NOV

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      Query Match
      48.1%; Score 39; DB 1; Length 381;

      Best Local Similarity 66.7%; Pred. No. 19;
      Antches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

      Qy 1 DELLAALGYKVR 12 1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1
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Search completed: December 19, 2001, 17:10:29 Job time: 175 sec

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Q9enkS porcine rep
Q9enkS porcine rep
Q98w5 porcine rep
Q98w5 porcine rep
Q9dln9 porcine rep
Q9dln9 porcine rep
Q9dln8 eropyrum p
Q9ydl neisseria m
Q9jwd2 neisseria m
Q9jwd1 neisseria m
Q9jsz8 neisseria m
Q9jsz8 neisseria m
Q9jsz8 pseudomonas
Q9jkG xytlalla fas
Q9lc55 pseudomonas
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
NCBI_TaxID-4565;
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SEQUENCE FROM N.A.
MEDILINE-99347734; PubMed=10421366;
Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,
Flintham J.E., Beales J., Fish L.J., Worland A.J., Pelica F.,
Sudhakar D., Christou P., Snape J. W., Gale M.D., Harberd N.P.;
"'Green revolution' genes encode mutant gibberellin response
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09enk5
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modulators.";
Modure 400:256-261(1999).
EMBL; AJ242531; CAB51555.1; -.
EMBL; AJ242531; CAB51555.1; -.
AMM; F2BAC34996D0A84F CRC64;
AMM; F2BAC34996D0A84F CRC64;
AMM; F2BAC34996D0A84F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
GIBBERELLIN RESPONSE MODULATOR:
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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ilarity 100.0%; Pred. No. 2.2e-05;
Conservative 0; Mismatches 0;
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P91577
Q06503
Q916C5
Q912R2
Q9PF80
           Q9YN01
Q9J7C0
Q9ENK5
Q9E8M9
                                                                              099AV5
09DLN9
09DLP1
09DLP0
09DLN8
080476
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Q9YAH8
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030707
09K0Y1
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Q9RGR6
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hes 17; Conserv
Query Match
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Ogg1813 arabidopsis
Ogg181 homo sapien
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09wjb3 porcine rep
09wbq4 porcine rep
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108.256 Million cell updates/sec
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                                                                                             ; Search time 22.97 Seconds
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                                                                                                                                                                                                                                                                               473505
                           Compugen Ltd
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q23724
Q9LQT8
Q9SRP9
Q23725
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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Theologis A., Ecker J.R., Palme C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palme C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

R. Bueller E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

R. Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H.,

R. Chung M.K., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hujzar L.,

R. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

R. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

R. Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

R. Langin-Hooper S., Liu Z.A., Luros J.S., Matti R., Marziali A.

R. Lin X., Liu S.X., Liu Z.A., Luros J.S., Matti R., Marziali B.,

R. Militscher J., Miranda M., Nayyen M., Nierman W.C., Osborne B.I.,

R. Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Zallon L.J., Tambunga G., Toriuni M.J., Town C.D.,

Utterback T., Van Aken S., Vaysberg M., Vysotskała V.S., Walker M.,

R. Sequence and analysis of chromosome 1 of the plant Arabidopsis

T. Tahliana.
                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophytá; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
Sato S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (ANG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70; DB 10; Length 511;
Pred. No. 0.0013;
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AI391150; CACO1893.1; - OF6CE0BD13403C35 CRC64;
SEQUENCE 523 AA, 57326 WW; OF6CE0BD13403C35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 408:816-820(2000).
EMBL; AC020665; AAG52171.1; -.
SEQUENCE 511 AA; 56754 MW; 1E60071697C92A9F CRC64;
  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GIBBERELLIN REGULATORY PROTEIN, PUTATIVE.
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Last sequence update)
Last annotation update)
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82.4%; Pred. No. 0.0014;
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Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
MEDLINE-21016719; Pubmed-11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Best Local Similarity 82.4'
Matches 14; Conservative
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                          Ogawa M., Kusano T., Katsumi M., Sano H.;
"Rice gibberellin-insensitive gene homolog, OsGAI, encodes a nuclear-
localized protein capable of gene activation at transcriptional
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                                                         Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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MEDLINE=99347734; PubMed=10421366;
Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,
Flintham J.E., Beales J., Fish L.J., Worland A.J., Pelica F.,
Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;
"'Green revolution' genes encode mutant gibberellin response
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EMBL; AB030956; BAA90749.1; -.
SEQUENCE 625 AA; 65406 MW; 034FF02719D42E97 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
GIBBERELLIN RESPONSE MODULATOR (FRAGMENT).
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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STRAIN-CV. NIPPONBARE;
MEDLINE-20179680; PubMed-10713441;
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EMBL; AJ242530; CAB51557.1; -.
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Cheur R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Theologis A., Ecker J., Theologis A., Ecker J., Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AC006917, AAF79228 I; SEQUENCE 533 AA; 58926 MW; 646486C129D79528 CRC64;
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82.4%; Pred. No. 0.0014;
Live 2; Mismatches 1; Indels
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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MEDLINE-98051192; PubMed=9389651;
MEDLINE-98051192; PubMed=9389651;
MEDLINE-98051192; PubMed=9389651;
Murphy G.P., Harberd N.P.;
"The Arabidopsis GAI gene defines a signaling pathway that negatively regulates gibberellin responses.";
Genes Dev. 11:3194-3205(1997).
EMBL; Y15193; CAA75492.1; ---
Mendel; 24070; Arath;3051;24070.
SEQUENCE 532 AA; 58789 MW; 4AF4BC6EC4265503 CRC64;
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MEDLINE-97379310; Pubmed-9237632;
Truong H.N., Caboche M., Daniel-Vedele F.;
Truong H.N., Caboche M., Daniel-Vedele F.;
Sequence and characterization of two Arabidopsis thaliana cDNAs isolated by functional complementation of a yeast gln3 gdh1 mutant.";
FEBS Lett. 410:213-218(1997).
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales, Brassicaceae; Arabidopsis.
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Mendel; 24146; Arath;3051;24146.
SEQUENCE 532 AA; 58789 MW; 17AC719CA8072239 CRC64;
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                                                                                            Query Match
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                                                                                                                                                                                                                       Q9SLH3
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065367
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                                                                                                                 Matches
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Q9SLH3
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta:
Spermatophyta: Magnollophyta: eudicotyledons; core eudicots: Rosidae;
eurosids II; Brasslcales; Brasslcaceae; Arabidopsis.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                          Gaps
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                                           Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Ronding C.M., Koo H., Fujil C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nerman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T21P5 genomic sequence.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC009895; AAF01590.1;
EMBL; AC009895; AAF01590.1;
C4D18D5951D95634 CRC64;
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                                                                                                                                                Score 70; DB 10; Length 547, Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Peng J., Carol P., Richards D.E., King K.E., Cowling R.J. Murphy G.P., Harberd N.P.; Genes Dev. 0:0-0(0). EMBL: Y15194; Y15194; Y15194; Y15194; Arath; 3051.24071. SEQUENCE 587 AA; 64006 MW; F6F6C7738EE7DCA9 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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2; Mismatches
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                                                                                                                                                                         Mismatches
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Truong H.N., Caboche M., Daniel-Vedele F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.4%; Score 70;
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                                                                                                                                                Query Match
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                               DELLAALGYKVRASDMA 17
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Matches 14; Conservative
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                      SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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NCBI_TaxID=3702;
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STRAIN-CV. COLUMBIA,
MEDLINE-20083487; PubMed-10617197;
MEDLINE-20083487; PubMed-10617197;
MEDLINE-20083487; PubMed-10617197;
Lin X., Kaul S., Rounnaley S.D., Shea T.P., Benito M.-I., Town C.D.,
Eujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.Y., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome II of Arabidopsis thaliana.";
Nature 402:761-766(1999).

EMBL, ACO05560; AAG67333.1; -.

SEQUENCE S87 AA; 64035 MW; FC92E7F9408072AA CRC64;
Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AT2G01570.
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Last sequence update)
Last annotation update)
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Q45645;
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                                                           "Cloning of the Arabidopsis thaliana RGA-like gene, a putative member of the VHID domain transcription factor family."; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ224957; CAA1242.1;
Mendel; 29006; Arath;3051;29006.

Interpro; IRMO1680; WA40.

SMART; SM00320; WD40; 1.

PROSITE; PS50082; WD_REPEATS_2: 1.

PROSITE; PS50082; WD_REPEATS_2: 1.

Repeat; WD_repeat.

SEQUENCE 662 AA; 73126 MW; 958AB73D42121CA8 CRC64;
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Fubuta M., Inazawa J., Torli T., Tsuzuki K., Shimada E., Habuchi O.;
"Moolecular cloning and characterization of human keratan sulfate
Gal-6-sulfotransferase."
J. Biol. Chem. 272:32321-32328(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Washaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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MEDLINE=99168906; PubMed=10049591;
L1 X., Tedder T.F.;
LG T. Tedder T.F.;
CHST1 and CHST2 sulfotransferases expressed by human vascular endothelial cells: CDNA cloning, expression, and chromosomal localization.";
Genomics 55:345-347(1999).
EMBL; U65637; AAC28776.1; --
EMBL; AB003791; BAAC4840.1; --
EMBL; AF090137; AAD19878.1; --
                    Sanchez-Fernandez R., Ardiles-Diaz W., van Montagu M., Inze D.,
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Pred. No. 0.0018;
1; Mismatches 2; Indels
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CHONDROITIN-6-SULFOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Atherosclerosis: cell biology and lipoproteins.";
Curr. Opin. Lipidol. 7:0-0(1996).
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Best Local Similarity 82.4%;
Matches 14; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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SEQUENCE 4
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Marasco R., Varcamonti M., Ricca E., Sacco M.;
"A new Bacillus subtilis gene with homology to Escherichia coli prc.";
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DB 4; Length 411; 27;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
0RFRM1 DNA.
                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=1423;
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Pred. No. 32;
4; Mismatches
                                   4; Mismatches
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 Score 44;
Pred. No. 2
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EMBL; X98341; CAA66987.1; -.
InterPro; IPR001478; PD2.
InterPro; IPR003581; TSPC.
Pfam; PF00595; PD2; 1.
PROSITE; PS50106; PD2; 1.
54.3%;
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                                   8; Conservative
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378 QVLAQLGYKIAASE 391
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SMART; SM00245; TSPC; 1
                                                                       2 ELLAALGYKVRASD 15
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Sequence

Description

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AJ342531 Triticum
AX005805 Sequence
AX005805 Sequence
AX005807 Sequence
AX00580 Sequence
AX00581 Sequence
AX00515 Sequence
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1 (bases 1 to 51)

Harberd, N.P. and Peng, J.

Genetic control of plant growth and development Patent: WO 9909174-A 105 25-FEB-1999;

HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)

Location/Qualifiers

1. 51
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Sequence 105 from Patent WO9909174.
AX005896
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AC006917
AX005865
MMULGENES
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AB057426
ATA224957
ATK3M16
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ATAC009895
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ATY15193
AE005134
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          Length
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DEFINITION
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TITLE
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591.376 Million cell updates/sec
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                                                                    ; Search time 1422.71 Seconds
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AE005134 Halobacte

278205 Bovine herp

24-AUG-2000

/organism="Triticum aestivum"

source

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/organism="Triticum aestivum"
/db_xref="taxon:4565"
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Sequence 14 from Patent WO9909174.
AX005805
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Nature 400 (6741), 256-261 (1999)
Pooideae; Triticeae; Triticum.
1 (bases 1 to 1872)
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/note="GAI ortholog"
/codon_start=1
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Poalees; Poaceae; Pooldeae; Triticaee; Triticaee; Triticum.

1 (bases 1 to 453)

Harberd, N.P. and Peng, J. Genetic control of plant growth and development Patent: WO'9909174-A 66 25-FEB-1999; Patent: WO'9909174-A 66 25-FEB-1999;

HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
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Triticum aestivum rht-Dla gene for gibberellin response modulator.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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gibberellin response modulator; rht-Dla gene.
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lilarity 100.0%; Pred. No. 7.8e-05;
Conservative 0; Mismatches 0;
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YEGEALLARTVERFEPOPDSSLLAAFADLLHAHFYEGOPYLKFAFANQALLEAFAG
CRRVHVVDFGIKQGMQMPALLQALALRPGGPPSFRLTGVGPPQPDETDALQQVGWKLA
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EAEKYLGYRAVRANPRATVYVEQEANINSGTFLDFFFESLHYSTMFDFBESLEGSSGGG
PSEVSSGAAARAARAADAGTDQVNSEYVLGRGJORVVACEGAERFERHETLAGMRRLGNA
GFETVHLGSNNYKQASTLLALFAGGDGYKVEEKEGCLTLGWHTRPLIATSAWRLAGP*
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1 (bases 1 to 2125)
Harberd, N.P. and Peng, J.
Febentic control of plant growth and development Patent: WO 990174-A 14 25-FEB-1999; HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Peng, J., Richards, D.E., Hartley, N.M., Murphy, G.P., Devos, K.M., Flintham, J.E., Beales, J., Fish, L.J., Worland, A.J., Pelica, F., Sudhakar, D., Christou, P., Snape, J.W., Gale, M.D. and Harberd, N.P., Green revolution, genes encode mutant gibberellin response
                                                                                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 1872)
Richards, D. E.
Direct Submission
Submitted (25-MAY-1999) Richards D. E., Molecular Genetics, John Innes Centre, Colney Lane, NR4 7UJ, UNITED KINGDOM
Location/Qualifiers
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Harberd,N.P., Peng,J. and Richards,D.E.
Green revolution genes encode mutant gibberellin response
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bread wheat.
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 (bases 1 to 324)
Harberd, N. P. and Peng, J.
Harberd, N. P. and Peng, J.
Harberd, WO 9909174-A 76 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 51; Conservative 0; Mismatches 0;
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Pred. No. 0.00032;
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                                                                                                                                                                                ch 100.0%; Score 51; DB 6; Similarity 100.0%; Pred. No. 4.8e-05; 51; Conservative 0; Mismatches 0;
Location/Qualifiers
1. 2125
/organism="Triticum aestivum"
/db_xref="taxon:4565"
1. 768 c 723 g 309 t
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RESULT 7 AX005803 LOCUS DEFINITION

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AUTHORS REFERENCE

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LGYKVRSSDMADVAQKLEQLEMAMGMGGVSAPGAADDGFVSHLATDTVHYNPSDLSSW
VESMLSELNAPLPPIPPAPPARHASTSSTVTGGGGSGFFELPAAADSSSSTYALRPI
SLPVVATADPSAADSARDTKRMRTGGGSTSSSSSSSSLGGGASRGSVVEAAPPATQG
                                                                                                                                                                                                                                                                                                         AAAANNPAVEVVVVDTQEAGIRLVHALLACAEAVOOENFAAAEALVKOIPTLAASQGG
AMRKVAAYFCEBLARRVYRFRERDSTULDAAFADLLHAHFESGSPLKFAHFTHAQAI
LEAFAGCHRVHVDDEGIKQGMQWPALLALRPGGEPSFRLTGVGEPQPDETDALQO
VGWKLAQFAHTIRVDFQYRGLVAATLADLEPPHLQPEGEADANEEPEVIAVNSVFELH
                                                                                                                                                                                                                                                                                                                                                                                                RLLAQPGALEKVLGTVHAVRPRIVTVVEQEANHNSGSFLDRFTESLHYYSTMFDSLEG
GSSGQAELSPPAAGGGGGTDQVMSEVYLGRQICNVVACEGAERTERHETLGQWRNRLG
RAGFEDVHLGSNAYKQASTLLALFAGGDGYRVEEKEGCLTLGWHTRPLIATSAWRVAA
                                                                                                                                                                      /protein_id="BAA90749.1"
/db_xref="GI:6970472"
/translation="MKREYQEAGGSSGGGSSADMGSCKDKVMAGAAGEEEDVDELLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Shermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; I to 12249; Buell, C.R., Yuan, Q., Ouyang, S., Moffat, K.S., Hill, J.N., Tanner, M., Burgess, S., Hance, M., Shvartsbeyn, M., Tsitrin, T., Riggs, F., Hislao, J., Zismann, V., Bluut, S., Pal, G., VanAken, S.E., Utterback, T.R., Feldblyum, T.V., Quackenbush, J., Salzberg, S.L., White, O. and Fraser, C.M.
Oryza sativa chronosome 3 BAC OSJNBb0022E02 genomic sequence Unpublished
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Submitted (03-MAY-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org
On Apr 20, 2001 this sequence version replaced g1:13605985.
Address all correspondence to:rice@tigr.org
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Submitted (25-JAN-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
3 (bases 1 to 122497)
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Medical Center Dr, Rockville, MD 20850, USA
4 (bases 1 to 122497)
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Pred. No. 0.002;
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'dev_stage="seedling"
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                                                                                                             /note="GAI homolog
                                                                                                                                                         /product="OsGAI"
         /gene="OsGAI"
216. 2003
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                                                                                    /gene="OsGAI"
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1 (bases 1 to 770)
Harberd,N.P. and Peng,J.
Genetic control of plant growth and development
Patent: WO 9909174-A 12 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
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Mikhliro Ogawa, Nara Institute of Science and Technology, Plant
Molecular Breeding; Takayama 8916-5, Ikoma, Nara 630-0101, Japan
(E-mail:m-ogawa@bs.aist-nara.ac.jp, Tel:+81-743-72-5652,
    Gaps
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Rice gibberellin-insensitive gene homolog, OsGAI, encode
nuclear-localized protein capable of gene activation at
                                             DB 6; Length 770;
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Oryza sativa mRNA for OsGAI, complete cds.
AB030956
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Pred. No. 0.0029;
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Squence 12 from Patent W09909174.
AX005803.1 GI:9928800
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/db_xref="taxon:4530"
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/cultivar="Nipponbare"
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94.0%;
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSGAI
  49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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DEFINITION

RESULT AB030956

Locus

VERSION KEYWORDS SOURCE ORGANISM

EFERENCE AUTHORS TITLE

MEDLINE EFERENCE AUTHORS

JOURNAL

TITLE JOURNAL

source

ATURES

ö

Gaps

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.15274,15344. .16687,16818. .17803,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(14168. 15023-15131. 15274,15344. 16687,16818. 17803, 17887. 18048,18262. 18366)
/gene="OSJNBb00022E02.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YECGGLERESLADECNISYNHICGSVODEANWHSRLCHINFGLMSRLASMCLIPKES
IVGSKCHSCVOSKOPRPHKAAEERNILAPLISDLCEMNGVITKGRRYEFTLID
DATRECYVILLKTKDEALDYFKIYKAEERNILAPLISDLCEMNGVITKGRRYEFTLID
DATRECYVILLKTKDEALDYFKIYKAEVENOLDRK IKRLRSDRGGEFFSNEFDLFCEE
HGIIHERTPPYSPESNGIAERNRTJTDLVNAMLDTAGLPKAMMGEALLTSNHTUNKY
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TEHTHELVSEEDVSEAPRRSKRORTAKSFGDDFTVVIVDDTPKSISRAYASPDADVWR
EAVRSEMDSIIANGTWEVTERPYGCKPVGCKWVFKKLRPDASHGLLVHQMDVKTAFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGELDEEIYMDQPDGFVVEGGEGKVCKLLKSLYGLKQAPKQMHEKFDKTLTSAGFAVN
EADKCYYYRHGGGEGVILCLYVDDILIFGTNLEVINEVKSFLSQNFDMKDLGVADVIL
NIKLIRGENGITLLQSHYVEKILNRFGYIDSKPSPTPYDPSLLLRKNKRIARNQLEYS
                                                                                                                                     RVKSKPTVDLKIVFLPLLAFEVIILADNFRMCRALMPGDEESMSDEAIWETLPHFWVA
ISMVFLIAATTFTLLKLSGDVGALGWMDLFINYGIAECFAFLVCTRWFNPMIHKSPNP
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VLTAEQQKQFEEATTLFVGCILSVLGDRLVEVYMHMTDAKELMDALNTKFGATDASND
LYIMEQFHDYKMADNRSVVEQAHEIQTMAKELELLKCVLPDKFVAGCIIAKLPPSWRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGTALKHKRQEYSVEGLIASLDVEEKAREKDAASKGDGGSSANVYHKAONKSKGKYK
AQQTTNFKKQKKNNNNPNQDERTCFVCGQVGHLARKCPQRKGMKAPAGGTSKSANVTI
GNTGDGSGYGRTGFHRPNGEWVTCFCSWCWHGRSEVYFGKDRAAEERAACPFYRQESC
                                                                                                                                                                                                                                  EGTPPSAQYIPIFALFSPLFILGGAGVLFSLARLLEKVVLLLRNGPVSPNYLTISSKV
RDCFAFLHRGSRLLGWWSIDEGSKEEGARLFYTESTGYNTFCGYPPEVVRKMPKRDLA
EEVWRLQAALGEQSEITKCTKOEFERLONEKVLCRICYEGEICMVLLPCRHRTLCKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OIIGSLMYLASATRPDISFAVSKLSRFTSNPGDDHWRALERVMRYLKGTVELGLHYTG
YPAVLEGYSDSNWISDVDEIKATSGYVFTLGGGAVSWRSCKQTILTRSTWEAELTALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATVEAEWLRDLLMDLPVVEKPTCEKTIEVCQEIKKLRSYNVGLHPNSEKPGRSLHEG
TITKCDRQCIEGDGFETHSILEGTHLCELDCWSQSMKILGESSRKLTKDLGV"
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WIIFIPLWLFHGIVARGRFSMPAPSLPHGRHWAPCHSIVAAPLLIAFELLLCIYLESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTTRTVLLSEYSDSGHDNSGRNGAVAGVVGHGVGAGGRGLHGYI
ACAVVLLASTPYAPLHIQGDELQHGVWTAKDDCRWRQAPAWDVDYEPTSNDASVPNS"
complement(22507. .22529)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="OSJNBb0022E02.12"
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GI:4234852 (2ea mays)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative gag-pol polyprotein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
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complement(12558. 12580)

/rpt_family="(GA)n"

join(<14168. 15023,15131. 152'

17887. 18048,18262. >18366)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="predicted by fgenesh"
                                                                                                                                                                                                                                                                                                                                  SDKCKKCPICRVPIEERMPVYDV" complement(12328. .12420)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="AT_rich"
complement(20459. .20487)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(18822. .18858)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="(CAGGC)n"
complement(19612, .19640)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(TA)n"
complement(22544. .22588)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <21271. .>21576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /qene="OSJNBb0022E02.13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="AT_rich" <21271. .>21576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .21576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14168. .18366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                     Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genesan+ (Chris Burge, http://www.softberry.com/), http://CCR-081.mit.edu/GENGAN.html), GeneMarkHWM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mperteactigr.cog), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tg1.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Simple repeats are hittp://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are hittp://fenome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are hittp://fenome.wustl.edu/eddy/tRNAscan-SE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEDNTENGEDDTNGAARYFESTTARAQNOTTGVAVAVREEL

complement(join(<5240. 5517,5605. 5664,6132. 6212,
6314. 6383,6539. 6613,6693. .6699,7177. 7426,7506. 7551,
8773. 8842,9564. .9633,11257. .11341,11440. .11524,
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/gene="GSJNBD0022E02.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /grammars.complement(join(5439. .5517,5605. .5684,6132. .6212,
complement(join(5439. .5517,5605. .5684,6132. .6212,
6314. .6383,6539. .6613,6693. .6898,7177. .7426,7506. .7551,
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11608. .11698,12255. .12388))
//gene="OsJNBb0022E02.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mentkaaplusssprsylslpaavdprptlrappllhpglsvap
SCRTRSSGTLEWTPVKTLALMAKVVVIDDGWSHSVSAFQKWAVLAENLAGSYFVAATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:13937302"
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clone OSJNBb0022E02 is from Oryza sativa chromosome 3 orientation of the sequence is from SP6 to 77 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //oote="predicted by fgenesh"
complement(1271, .1579)
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/qene="OSJNBb0022E02.18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .>1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="C944"
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24 - AUG - 2000

mRNA gene

CDS

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                      Enkaryota: Widiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticae; Triticum.

1 (bases 1 to 200)
Harberd, NP. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 69 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 others
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Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 16 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
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                                             PAT
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Pred. No. 0.016;
0; Mismatches
                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                                                                                                                                                                          /note="n is any nucleotide"
172
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188
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58 c 84 g 27 t
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                                      Sequence 69 from Patent WO9909174. AX005860
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AX005807
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/db_xref="taxon:4577"
82 c 123 g
                                                                                            AX005860.1 GI:9928855
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Best Local Similarity 93.8%;
Matches 45; Conservative
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                                                            DEFINITION
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                                                                           ACCESSION
VERSION
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TITLE
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               RESULT 1.
AX005860
LOCUS
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           /tianslation-"MAAGSGARAVGDNGGGCPPAPASLPLPPRHPSSPRRTPA
SPIGLLPPRRICKOYSTGSLPESAAGHAVAPPSPSRRRGADADGESVLGLSSBAAV
WOAQARSGCEGNBESMAVLACAPYAGDLALAKGERTHGCCVMKGYTHGYTTUSL
VCMYGKLGEMDNAKRAFRDATEKNIVTWNTLITSYATAGLCDEALDVLAQMEQIGGTV
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 725)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 19 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 0.00059;
0; Mismatches 3; Indels 0;
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                                                                                                                                                                         /product-"hypothetical protein"
/protein_id-"AAK50123.1"
/db_xref-"GI:13937292"
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Pred. No. 0.0056;
0; Mismatches 3
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459
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226 c 276 g 119 t
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    .725
    /organism="Oryza sativa"
    /db_xref="taxon:4530"

/rpt_family="AT_rich"
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93.9%;
                                                                                                                                                                                                                                                                                                        88.6%;
94.0%;
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Matches 47; Conservative
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Best Local Similarity
Matches 46; Conserv
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RESULT 10 AX005810 LOCUS DEFINITION

OURCE ORGANISM

ACCESSION VERSION KEYWORDS

source

EATURES

EFERENCE AUTHORS TITLE JOURNAL

BASE COUNT ORIGIN

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Gaps

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24-AUG-2000

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GGAMRKVAAYFGBALARRYYRERPPDSSLLDAAFADLHAHFYESCPYLKFAHFTAN
QAILERFAGCRRYHVVDFGIKGMQWAALLQALALREGGPPSFRLTGVGPPQPDETDA
LOOGWILLAQPEAHTIRVDFQYRGLVAATLADLEPFMLQPEGDTDDEPEYIAVNSYFE
LHRLLAQPGALEKVLGTVARVRPRIYVVVQEANHNSGTFLDRFTESLHYXSTWFDSL
EGAGAGSGOSTPLASPAAAGGTPQVMSEYYLGRQICNVYACEGARRFTEHETLGQWRSR
LGGSGGFPAPYHLGSNAYKQASTLLALFAGGDGYRVEEKDGCLTLGWHTRPLIATSAWRY
                                                                                                                                                                                                  VESMLSELNAPPAPLPPATPAPRLASTSSTVTSGAAAGAGYFDLPPAVDSSSSTVALK
PIPSPVAAPSADPSTDSAREPKRMRTGGSSTSSSSSSSSMDGGRTRSSVVEAAPPAT
QASAAANGPAVPVVVVDTQEAGIRLVHALLACAEAVQQENFSAAEALVKQIPMLASSQ
                                                                                                                                                               /translation="MKREYQDAGGSGCDMGSSKDKMMAAAAGAGEQEEEDVDELLAAL
GYKVRSSDMADVAQKLEQLEMAMGMGGVGGAGATADDGFVSHLATDTVHYNPSDLSSW
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1 (bases 1 to 225)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development Patent: WO 9909174.A 15 25-FEB-1999;
HARBERD NICHOLAS PALL, (GB); PENG JINRONG (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 GATGAGCTGCTGGCCGCGCTCGGGTACAAGGTGCGTTCGTCGGATATGGCG 358
                                                                                     /codon_start=1
/product="qibberellin response modulator"
/protein_id="CAB51557.1"
/db_xref="G1:5640155"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.0%; Score 39.8; DB 8;
86.3%; Pred. No. 0.071;
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Sequence 15 from Patent WO9909174.
AX005806
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817 c 737 g
                                                                      /note="GAI ortholog"
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Best Local Similarity 86.3%;
Matches 44; Conservative
               /gene="d8"
1. .>1890
                                                  /gene="d8"
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ORIGIN
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                                   CDS
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Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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Peng,J., Richards,D.E., Hartley,N.M., Murphy,G.P., Devos,K.M., Filntham,J.E., Beales,J., Fish,L.J., Worland,A.J., Pelica,F., Sudhakar,D., Christou,P., Snape,J.W., Gale,M.D. and Harberd,N.P., Green revolution' genes encode mutant gibberellin response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-MAY-1999) Richards D.E., Molecular Genetics, John Innes Centre, Colney Lane, NR4 7UJ, UNITED KINGDOM Location/Qualifiers
1. .1890
//organism="Zea mays"
/db_xref="taxon:4577"
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                                                    Gaps
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                                                                                     Length 302;
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                                                    Indels
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Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 17 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
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             Score 39.8; DB Pred. No. 0.13;
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                                                  0; Mismatches
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Sequence 17 from Patent WO9909174.
AX005808
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/db_xref="taxon:4577"
1 121 c 139 g
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1 Similarity 86.3%;
44; Conservative
             78.0%;
86.3%;
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                                                  44; Conservative
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             Query Match
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ORGANISM
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ORIGIN
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AX005808
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LOCUS
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21

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Arabidopsis thalia DNA sequence obtai Arabidopsis SCL ES A. thaliana transc Arabidopsis thalia Arabidopsis thalia

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Run on:

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New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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DNA sequence obtai
Wheat Rht clone 5a
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306.596 Million cell updates/sec
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                                                                                                                                  ; Search time 142.61 Seconds
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Compugen Ltd.
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Copyright (c) 1993 - 2000
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Listing first 45 summaries
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us-09-485-529-105.rng

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibitnon is antegonised by glabbarellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with glabberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild type, the dwarfing being glabberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit glabberellin blosynthesis, such as paclobutazol, e.g. to allow use of a glabberellin blosynthesis inhibitor to keep weeds
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                dwarf but let crop plants grow tall. The present sequence is derived from the wheat rht gene.
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                                                                                                                                                                                                                                                                                                        100.0%; Score 51; DB 20; 100.0%; Pred. No. 5.6e-08;
                                                                                                                                                                                                                                                              Sequence 51 BP; 7 A; 16 C; 21 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                      0; Mismatches
   Claim 3; Page 53; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX36263 standard; DNA; 453 BP
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Best Local Similarity 100.
Matches 51; Conservative
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Tritiuum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by the plant. This growth inhibition is antagonised by is because it is a conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin blosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents
may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was obtained after partially sequencing wheat Rht clone 14al.
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                                                                                                                                                                                                                                                     Sequence 453 BP; 85 A; 136 C; 158 G; 67 T; 7 other;
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100.0%; Pred. No. 6.2e-08;
ive 0; Mismatches 0;
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Sequence 2125 BP; 325 A; 768 C; 723 G; 309 T; 0 other;

The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants

New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype

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Richards

Harberd NP, Peng J, WPI; 1999-181040/15

BIOSCIENCE LTD

(PLAN-) PLANT

Disclosure; Fig 2b(9); 88pp; English.

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       Length 2125;
                                                                                                                                                                          0; Indels
                                                                                                                                         1 gacgagetgetggeggegetegggtacaaggtgegegeeteegacatggeg
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Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 51; Conservative 0; Mismatches 0;
100.0%; Score 51; DB 20;
100.0%; Pred. No. 6.5e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composite DNA sequence of wheat Rht gene.
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                                Local Similarity 100.
es 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum.
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       Query Match
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AAX36275

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence was dwarf but let crop plants grow tall. The present sequence was
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                                                                                                                                                 gene; homologue; Triticum aestivum; wheat; growth inhibition; agonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
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                                                                                                                DNA sequence obtained after sequencing wheat Rht clone 5al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gacgagctgctggcggcgctcgggtacaaggtgcgcgcctccgacatggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 GNCGNGCTGCTGCGGCGCGCCTCGGTACAAGGTGCGCCCCCCCCACATGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice EST D39460 sequence, homologous to wheat Rht gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Richards DE;
                 BP.
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96.1%;
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AAX36273/c
ID AAX36273 standard; DNA; 324
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Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-181040/15
                                                                                                                                                                                paclobutrazoī; ss.
                                                                                                                                                                                                                 Friticum aestivum.
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                                                AAX36273;
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AAX36277
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                                   07-AUG-1998;
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Matches
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Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; rice; expressed sequence tag; EST; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
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4.6e-06;
3;
                                                                                                                                                                                                                                                                     DE;
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                                                                                                                                                                                                                                                                     Richards
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Matches 47; Conservative
                                                                                                                                                                                                                                                                   Harberd NP, Peng J,
                                                                                                                                                                                                                                                                                                   WPI; 1999-181040/15
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                                                                    Oryza sativa
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                                                                                                  W09909174-A1
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Trilicum Asstivum, inhibit growth of the plant. This growth inhibition is antagonised by gluberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by the product scan be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gluberellin. Insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gluberellin blosynthesis, such as paclobutrazol, e.g. to allow use of a gluberellin blosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence represents the partial cDNA sequence of rice AAD39460 (a wheat Rht gene homologue).
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                                                                                                                                                                       New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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Richards DE;
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WPI; 1999-181040/15

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth inhibition is antagonised by growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence was dwarf dwarf but let repartially sequencing wheat Rht clone 14al.
                  which
                                                                              is
New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
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                                                                                                                                                                                                                                           Disclosure; Fig 2b(12); 88pp; English
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ö Gaps ö Score 43.2; DB 20; Length 200; Pred. No. 1.9e-05; 0; Mismatches 3; Indels 0 gactatctgctggcggcgctcgggtacaaggtgcgcgcctccgacagg 126 1 gacgagctgctggcggcgctcgggtacaaggtgcgcgcctccgacatg 48 Query Match 84.7%; Best Local Similarity 93.8%; Matches 45; Conservative σ 79 AX36281 ESULT

AAX36281 standard; DNA; 302

AAX36281;

16-JUL-1999 (first entry)

Partial sequence of the maize D8-1 allele.

gene; homologue; Triticum aestivum; wheat; growth inhibition; agonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; maize; ss antagonist;

Zea mays

WO9909174-A1

25-FEB-1999

98WO-GB02383. 07-AUG-1998;

97GB-0017192

13-AUG-1997;

(PLAN-) PLANT BIOSCIENCE LTD.

Richards Peng J, Harberd NP,

DE;

WPI; 1999-181040/15, P-PSDB; AAY02542.

New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype

Disclosure; Fig 11a; 88pp; English.

The specification describes polypeptides encoded by the Rht gene (and

yerowth of the plant. This growth inhibition is antagonised by globerellin. The products can be used to provide Rht expression in plants. Conferring a dwarf phenotype on a plant which is correctable by treatment with globerellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being globerellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit globerellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gliberellin biosynthesis, inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the partial sequence of the maize D8-1 allele. homologues) that, when expressed in Triticum Aestivum, inhibit

Sequence 302 BP; 52 A; 82 C; 123 G; 45 T; 0 other;

Gaps ö Length 302; Indels Score 39.8; DB 20; Pred. No. 0.00024; 0; Mismatches 78.0%; 86.3%; Query Match 78.0 Best Local Similarity 86.3 Matches 44; Conservative

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g δ

10 AAX36282

BP AAX36282 standard; DNA; 371

AAX36282;

(first entry) 16-JUL-1999 Partial sequence of the maize D8-2023 allele.

Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; maize; ss

Zea mays.

WO9909174-A1

25-FEB-1999

98WO-GB02383. 07-AUG-1998; 97GB-0017192. 13-AUG-1997;

(PLAN-) PLANT BIOSCIENCE LTD

Richards Harberd NP, Peng J,

DE;

WPI; 1999-181040/15. P-PSDB; AAY02543.

New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype

Disclosure; Fig 11c; 88pp; English.

The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Asstivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products growth or used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to

9

86.38;

Best Local Similarity

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin blosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin blosynthesis inhibitor to keep weeds dwarf but it et crop plants grow tall. The present sequence represents
e.g. to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence represents the partial sequence of the maize D8-2023 allele.
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homologue; Triticum aestivum; wheat; growth inhibition; t; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                              ö
                                                                                                                                              Length 371;
                                                                                                                                                                                                                                1 gacgagctgctggcggcgctcgggtacaaggtgcgcgcctccgacatggcg
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2255 BP; 334 A; 817 C; 737 G; 367 T; 0 other;
                                                                                         Sequence 371 BP; 56 A; 121 C; 139 G; 55 T; 0 other;
                                                                                                                                          78.0%; Score 39.8; DB 20;
86.3%; Pred. No. 0.00025;
.lve 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the maize lal genomic clone sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 9a; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize lal genomic clone seguence.
                                                                                                                                                                                                                                                                                                                                   AAX36280 standard; DNA; 2255 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                            Local Similarity 86.3
hes 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            paclobutrazol; maize; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-181040/15.
P-PSDB; AAY02541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antagonist;
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by its qibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with used to produce Rht mutant plants which are dwarfed compared with may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis annibitor to keep weeds dwarf but let crop plants grow tail. The present sequence represents the partial sequence of the wheat rht-10 allele.
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                                                                                                                                                                                                                                                                                                   >mologue; Triticum aestivum; wheat; growth inhibition;
gibberellin; dwarf phenotype; gibberellin biosynthesis;
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                                                                                            308 gatgagctgctggccgcgctcgggtacaaggtgcgttcgtcggatatggcg 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 416;
                                                              gacgagetgetggcggcgctcgggtacaaggtgcgcgcctccgacatggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 416 BP; 59 A; 168 C; 129 G; 60 T; 0 other;
Pred. No. 0.00026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.5%; Score 39; DB 20;
100.0%; Pred. No. 0.00045;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Partial sequence of the wheat rht-10 allele.
                               0; Mismatches
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                                                                                                                                                                           AAX36283 standard; DNA; 416
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                             44; Conservative
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                                                                                                                                                                                                                                                                                                      Rht gene; homologue;
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                                                                                                                                                                                                                                                                                                                                      paclobutrazol; ss.
                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum.
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Local Sim
39;
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                                                                                                                                                                                                                                                                                                                       antagonist;
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Matches
                               Matches
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RESULT

Length 2255;

DB 20;

Score 39.8;

78.08;

Query Match

complement (49..1745) Location/Qualifiers

(first entry)

*tag= a label= ORF1

2216..3937

/*tag= b /label= ORF2 3940..5481

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Clavulinic acid; clavulinate; antibiotic; beta-lactamase-inhibitor;
                                         S. clavuligerus cla gene region.
                                                                                             Streptomyces clavuligerus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38-OCT-1993;
                     13-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA2108113-A.
                                                                        cla gene;
 AAQ91580;
                                                                                                                 Key
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  Preparation of N-substituted azetidinone, useful as intermediate for clavulanic acid, by cyclisation of N-substituted aminopropanoic acid in presence of beta-lactam synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes an beta-lactam synthetase polypeptide. The enzyme is encoded by orf3 of the clavulanic acid biosynthesis cluster. This enzyme converts a beta-anino acid (formed from arginine and pyruvate) into the beta-lactam form, early in the clavulanic acid biosynthesis pathway. The beta-lactam synthetase enzyme is used for 2-aminopropanoic acid derivatives. The method is particularly used to make (25)-5-quanidino-2-(2-oxo-azetidin-1-yl)pentanoic acid from N2-(2-carboxyethyl)-(5)-arginine. (25)-5-quanidino-2-(2-oxo-azetidin-1-yl)pentanoic acid is an intermediate for clavulanic acid, a known inhibitor of beta-lactamase, used in combination with beta-lactam antibiotics for treatment of infections. More generally, N-substituted azetidinones are intermediates for other clavulams and
                                                                                         Beta-lactam synthetase; orf3; clavulanic acid biosynthesis cluster; beta-amino acid; beta-lactam; clavulanic acid biosynthesis; N-substituted azetidinone; clavulanic acid; beta-lactamase inhibitor; (2S)-5-guanidino-2-(2-ox-azetidin-1-yl)pentanoic acid; beta-lactam antibiotic; infection; clavulam; ss.
                                                                                                                                                                                                                                                                                                                            Thirkettle JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1542 BP; 190 A; 591 C; 557 G; 204 T; 0 other;
                                                                      encoding a beta-lactam synthetase enzyme.
                                                                                                                                                                                                                                                                                                                            Schofield CJ,
                                                                                                                                                                           Location/Qualifiers
4..1542
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 22; 31pp; English.
          AAZ60717 standard; DNA; 1542 BP
                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                               99WO-GB02301
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                                                  16-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                            Barton B, McNaughton HJ,
                                                                                                                                                         Streptomyces clavuligerus.
                                                                                                                                                                                                                                                                                                                                                WPI; 2000-182296/16.
P-PSDB; AAY68875.
                                                                                                                                                                                                                      WO200003581-A1
                                                                                                                                                                                                                                                                                   17-JUL-1998;
                                                                                                                                                                                                                                                              15-JUL-1999;
                                                                                                                                                                                                                                          27-JAN-2000
                               AAZ60717;
                                                                       DNA
AAZ60717
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complement (10998..12296)

/*tag= g /label= ORF7

/label= ORF4 /note= "cla gene"

.7588

/label= ORF3 5654..6595

*tag=

/*tag=

/*tag= e /label= ORF5

7895..9076

/label= ORF6

/*tag=

9241..10908

complement (12662. 13365)

/*tag= h /label= ORF8

/*tag= j /label= ORF10

93CA-2108113. 93CA-2108113

/label= ORF9

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A library of S. clavuligerus NRRL 5741 genomic DNA fragments (15-22 kb) constructed in cosmid pLAFR3 was screened for the cla gene using a probe based on a partial N-terminal sequence from the CLA enzyme. Isolated clone K6L1 included a 15kb fragment having the sequence given in AAQ91580 that included the cla gene (ORF4).
                                                                                                                                                                  WPI; 1995-207301/28.
P-PSDB; AAR77858; AAR77859; AAR77860; AAR77861; AAR77862; AAR77863;
AAR77864; AAR77865; AAR77866; AAR77867.
                                                                                                                                                                                                                                                                                                                                              Clavulanic acid biosynthesis enzymes and corresp. DNA - useful for biosynthesis of the antibiotic in Streptomyces hosts which do not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15079 BP; 2097 A; 5488 C; 5324 G; 2170 T; 0 other;
                                                                                     Paradkar AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig.2; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        naturally produce clavulanate
                                                                                     Jensen SE,
(UYAL-) UNIV ALBERTA
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Gaps

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37; Conservative

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Query¦Match Best Local Similarity Matches 37; Conserv

AAQ91580 standard; DNA; 15079 BP

AAQ91580 ID AAQ9 XX

RESULT

Length 1542;

Score 29.8; DB 21; Pred. No. 0.43;

58.4%;

0.43; Mismatches

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by globerellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by the conferring a dwarf phenotype on a plant which is correctable used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being globerellin-insensitive. Taller plants wild-type, the dwarfing being globerellin-insensitive. Taller plants the plant of interest. Plants may be made which are resistant to compounds which inhibit globerellin blosynthesis, such as paclobutrazol, e.g. to allow use of a globerellin blosynthesis, such as paclobutrazol, e.g. to allow use of a globerellin blosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence was obtained after partially sequencing wheat Rht clone 14al.
                                      ö
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                    Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
Length 15079;
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                                                                                                                                                                                                                                                                                                                  DNA sequence obtained after sequencing wheat Rht clone 14al.
                                                                                              21
                                      Indels
                                                                           3 cgagctgctggcggcgctcggggtacaaggtgcgcgcctccgacatggcg
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                                      12;
   DB 16;
Query Match 58.4%; Score 29.8; DB Best Local Similarity 75.5%; Pred. No. 0.47; Matches 37; Conservative 0; Mismatches
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                                                                                                                                                                                                        AAX36261 standard; DNA; 309 BP
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                                                                                                                                                                                                                                                                             16-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                         paclobutrazol; ss.
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Gaps

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57.6%; Score 29.4; DB 20; Length 309; 93.8%; Pred. No. 0.55; tive 0; Mismatches 2; Indels 0

tcgggtacaaggtgcgcctccgacatggcg 51

20 16

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Conservative

Query Match Best Local Similarity Matches 30; Conserv

Search completed: December 19, 2001, 22:25:14 Job time: 5581 sec

- Proceedings of the Company Company Angle (大き) (1985年) (198 $\sqrt{\chi^2}$

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NF099H09S
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NF072A05S
NF072A07S
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EST306157
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sf95f03.y
AV643605
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Sasaki, T., Miyao, A. and Yamamoto, K.
Rice cDNA from callus 1995
Unpublished (1995)
Unpublished (1995)
Unpublished (1995)
Nice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
Tel: 81-298-38-7441
Fax: 81-298-38-7468
 NF045B07I
                            MtBA31D06
                                          MtBA44B05
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AL233043 T
T22782 479
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AW694061
AW694064
AW696350
AW584593
AW584661
AA660952
BG647068
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BF424878
BI419902
AW267879
AW584431
                                          AL371425 | AW697326 | AW695914 |
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BE524828
                              AL369482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D39460 263 bp mRNA EST 11-N
RICSO803A Rice shoot Oryza sativa cDNA, mRNA sequence.
D39460
D39460.1 G1:568611
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/db_xref="taxon:4530"
/clone_lib="Rice shoot"
/note="Etiolated shoot (8 days old)"
64 c 116 g 35 t 2 others
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/organism="Oryza sativa"
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                                                                                               December 19, 2001, 16:58:38; Search time 1383.43 Seconds (without alignments) 396.142 Million cell updates,
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
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Best Local Similarity 94.0%;
Matches 47; Conservative
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Best Local Similarity 94.0%;
Matches 47; Conservative
                                          305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidaes; Oryzae; Oryza.

1 (bases 1 to 388)
Yamamoto, K. and Sasaki, T.
Rice cDNA from callus 1997
Unpublished (1997)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8002, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.
Location/Qualiflers
                                                                                                                                                                   C27475 388 bp mRNA EST 06-AUG-1997 C27475 Rice callus cDNA Oryza sativa cDNA clone C51976_1A, mRNA
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Sasaki, T. and Yamamoto, K.
Rice cDNA from immature leaf including apical meristem (2000)
Contact: Takuji Sasaki
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94.0%; Pred. No. 0.00071;
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Pred. No. 0.00072;
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/clone_lib="Rice callus cDNA"
/tissue_type="callus"
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/clone="E60220"
/clone="E60220"
/clone_lb="taxon:4520"
meristem (under short day condition)"
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M222715 Rice shoot Oryza sativa cDNA clone S0583, mRNA sequence.
AU222715 GI:15008327
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'.
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone="S0583"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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/note="Etiolated shoot (8 days old)"
136 c 176 g 65 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45.2; DB 10;
Pred. No. 0.00073;
0; Mismatches 3;
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Pred. No. 0.00073;
0; Mismatches 3;
                                                                                                                                                                                                    1. 399
/organism="Oryza sativa"
/strain="Nipponbare"
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179 g
                                                                                                                                                                                                     Email: gijzenm@em.agr.ca.
Location/Qualifiers
1...711
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Location/Qualifiers
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BE659954.1 GI:9985948
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207 c
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                                                  (bases 1 to 711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                   Glycine.
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                                                                                                                                                                                                                                                                                                                                                                                          Development of a genetically and physically anchored EST resource for barley genomics

L Unpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11199013.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAAGGG
High quality sequence stop: 587.
                                                                     BF268018 844 bp mRNA EST 09-MAR-2001
HV_CEG0019J17f Hordeum vulgare seedling green leaf EST library
HVCDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
BF268018
                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 844)
                                                                                                                                                                                                                                                                                                                           Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To see http://www.genome.clemson.edu/orders" 290 c 276 g 128 t
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Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Pred. No. 0.0011;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 GACGAGCTGCTGGCCGCGCTACAAGGTGCGGGCGTCCGACATGGCG 310
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1 gacgagetgetggeggegetegggtacaaggtgegegeeteegacatggeg
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/cultivar-"CI16155 (Mla13)"
/db_xref-"taxon:4513"
                                                                                                                                                                                        BF268018.2 GI:13263734
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92.2%;
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es 47; Conservative
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Hordeum vulgare
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/tissue_irp oracas.
/tissue_irp oracas.
/tissue_irp oracas.
/tissue_irp oracas.
/tissue_irp oracas.
/lab.host="E. coli strain XLOLR"
/note="Vector: pBK-CWV; Site_1: ECORI; Site_2: Xhol; This cDNA library was constructed from polyA+ enriched mRNA from green seed coats in mid to late developemental stage, average fresh weight 250 mper seed. Traces of pod and embryo tissue also present. Complementary DNA was synthesized from mRNA using an Xhol-poly(dT) linker-primer. ECORI adopters were ligated to the blunt-ended cDNA fragments and the products were digested with Xhor for directional cloning into lambda ZAP Express vector. This lambda library was amplified once using E. coli host strain XL1 Blue MRF'. Inserts were then subcloned by mass excision using ExAssist helper phage for strain XL1 blue MRF'. Inserts were then strain XL1 blue MRF'. Inserts were then strain XL1 blue MRF'. Inserts were then strain XL0 blue MRF'. Inserts were then strain XL0 blue XF.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                    Agriculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada NSV 4T3
TTE1: 519 457 1470
Fax: 519 457 3997
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1391 Sandford Street, London, Ontario, Canada N5V
Tel: 519 457 1470
Fax: 519 457 3997
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Contact: Gijzen M
                                                                                                                                        Harris, N., Chapman, B.P. and Gijzen, M. Gene expression in developing soybean seed coats Unpublished (2000)
Contact: Gijzen M
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88.0%; Pred. No. 0.019;
Live 0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Glycine max"
/cultivar="Harosoy 63"
/db_xref="taxon:3847"
/clone_lib="GmaxSC"
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41; Conservative
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Lotus japonicus
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                                                 /clone_ith="GmaxSC"
/tissue_type="Seed coats"
/tissue_type="Seed coats"
/tissue_type="Seed coats"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBK-CWV; Site_1: EcoRI; Site_2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA
from green seed coats in mid to late developemental stage
, average fresh weight 250 mg per seed. Traces of pod and
embryo tissue also present. Complementary DNA was
synthesized from mRNA using an XhoI-poly(dT)
linker-primer. EcoRI adopters were ligated to the
blunt-ended crom mRNA using an AnoI-poly(dT)
linker-primer. EcoRI adopters were ligated to the
blunt-ended crom mRNA using and the products were digested
with XhoI for directional cloning into lambda 2AP Express
vector. This lambda library was amplified once using E.
coll host strain XLI Blue MRF'. Inserts were then
subcloned by mass excision using ExAssist helper phage for
conversion into phagemid vector pBK-CWY in E. coli host
strain XLOLR."
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
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/db_xref="taxon:34305"
/db_xref="taxon:34305"
/clone="MwL069f02_r"
/clone="MwL069f02_r"
/clone="lb_"cus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="voctor: pBluescriptII SK-; Site_1: EcoRI; Site_2:
Xhol: isolate=Miyakojima MG-20"
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Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Loteae;
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from
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Pred. No. 0.26;
0; Mismatches 6;
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/organism="Glycine max'
                 /cultivar="Harosoy 63'
/db_xref="taxon:3847"
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DNA Res. 7 (2), 127-130 (2000)
20277479
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Best Local Similarity 87.0%;
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ORGANISM
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TITLE
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AV410222
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DB 10; Length 355;

69.8%; Score 35.6; DB 82.0%; Pred. No. 0.44;

Query Match Best Local Similarity

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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Loteae;
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/drganism="Lotus japonicus"

/db_xref="taxon:34305"

/clone="www005b04_r"

/clone="totus japonicus young plants (two-week old)"

/dev_stage="young plants (two-week old)"

/note="vector: pBluescriptis (two-week old)"

/note: isolate="vector: pBluescriptis (two-week old)"

/note: isolate="vecto
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Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
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Generation of 7137 non-redundant expressed sequence tags from
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Indels
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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DNA Res. 7 (2), 127-130 (2000)
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AV422153.1 GI:7776718
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82.0%;
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BE321891.2 GI:11964088
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BI419686.1 GI:15190709
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ilarity 78.4%;
Conservative
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1 173 c
Conservative
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Matches 40; Conserv
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               Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: yanakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                        /organism="Lotus japonicus"
/db_xef="teaxon:34305"
/clone="MWLOGleal_r"
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptil SR-; Site_l: EcoRI; Site_2:
XhoI: _isolate=Wiyakojima_MG-20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW720697 478 bp mRNA EST 19-APR-2000 LJNEST7h8rc Lotus japonicus nodule library 5 and 7 week-old Lotus japonicus cDNA-5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 478)
Colebatch, G., Freund, S., Trevaskis, B. and Udvardi, M.
Lotus japonicus root nodule ESTs: tools for functional genomics Unpublished (2000)
Contact: Udvardi MK
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Max Planck Institute of Molecular Plant Physiology
Am Muchlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
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Pred. No. 1.9;
0; Mismatches
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Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: udvardi@mpimp-golm.mpg.de
Seg primer: T7
High quality sequence stop: 478.
Location/Qualifiers
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illarity 78.4%;
Conservative
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Lotus japonicus
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ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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ACCESSI KEYWORI

Medicago truncatula Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago. week-old Lotus Lotus japonicus Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Pabaceae; Papilionoideae; Loteae; /dev_stage="5 and 7 week-old plants"
/note="Organ: Nodule; Vector: pSPORT1: Site_1: SalI;
Site_2: NotI; The library was prepared using mRNA
extracted from nodules of 5 and 7 week-old Lotus plants.
Nodules were induced by, and contained Mesorhizobium BE321891 372 bp mRNA EST 21-DEC-2000 NF045B07IN1F1058 Insect herbivory Medicago truncatula cDNA clone 1 (bases 1 to 586) Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M. Lotus japonicus root nodule ESTs: tools for functional genomics Unpublished (2000) Contact: Udvardi MK Gaps BI419686 586 bp mRNA EST 15-AUG-2001 LjNEST47e12r Lotus japonicus nodule library 5 and 7 week-old japonicus cDNA 5', mRNA sequence. /clone_lib="Lotus japonicus nodule library 5 and 7 week-old" ö Length 586; 119 GACGAGCTTCTCGCGGTGGTGGGTTACAAGGTGAGGTCATCAGACATGGCG 169 172 GACGAGCITCTCGCGGTGGTGGGTTACAAGGTGAGGTCATCAGACATGGCG 222 51 51 Max Planck Institute of Molecular Plant Physiology Am Muchlenberg 1, 14476 Golm, Germany Fax: 49 31 567 8250 Eamil: udvardiempimp-golm.mpg.de Seg primer: T7 High quality sequence stop: 586. 1 gacgagetgetggcggcgetcgggtacaaggtgcgcgcetccgacatggcg Indels 1 gacgagetgetggeggegetegggtacaaggtgegegeeteegacatggeg

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FEATURES

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                                 Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores , H.K., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stree="mature"
//dev_stree="mature"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                         Unpublished (2000)
0.0 Jul 14, 2000 this sequence version replaced gi:9195668
Contact: Korth Fathology
                                                                                                                                                                                                                                                                                                                 University of Arkansas J. 217 Plant Science Building, Fayetteville, AR 72701, USA Tel: 501 575 5191 East: 501 575 7601 Email: kkorth@comp.uark.edu Medicago Genome Initiative accession: MGI:S:23522 Insert Length: 798 546 Error: 0.00 Plate: 045 row: B column: 07 Seq primer: TCACACAGGAAACAGCTAATGAC.
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Medicago truncatula"
/db_xref="taxon:3880"
/db_xref="taxon:3880"
/clone="inseqt herbivory"
/tissue_type="local and systemic leaves"
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       (bases 1 to 372)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papliionoideae; Trifolleae;
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Bp 191 91006 EVRX cedex - France
Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-esfetoulouse.infa.fr Website:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [ (bases 1 to 458) Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Journet, E.P., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson, V. and Gamas, P. Medicago truncatula ESTs from nitrogen-starved roots
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/dev_stage="harvested after 3 days of N-starvation"
/note="Vector: pBluescript pSK; Site_1: EcoR1; Site_2:
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                                         /organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32.4; DI
Pred. No. 3.8;
0; Mismatches
                                                       /cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBA30E09"
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/clone="MtBA31D06"
Location/Qualifiers
                                                                                                                             /clone_lib="MtBA"
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78.0%;
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Best Local Similarity 78.0
Matches 39; Conservative
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XhoI; Plants were grown in an aeroponic chamber for 14 days on nitrogen-rich medium followed by 3 days on N-free medium. RNA was extracted from root tips (1-3 cm). cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zapXR vector from Stratagene and packaged using Giapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France)."
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Gaps ; 0 Query Match 63.5%; Score 32.4; DB 10; Length 458; Best Local Similarity 78.0%; Pred. No. 3.8; Matches 39; Conservative 0; Mismatches 11; Indels 0.

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58.4%; Score 29.8;
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Sequence 1, A
Sequence 5, A
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Sequence 1,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-07-916-901-5
US-08-336-408B-1
PCT-US91-00399-1
US-08-440-856A-1
PCT-US96-05611A-12
US-08-23-137-1394-1
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US-09-103-840A-2
US-09-103-840A-1
US-08-998-416-401
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US-09-385-028-1
US-09-117-853-1
US-09-248-335-39
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                                                                                                                                                                                                                                                                    351203 seqs, 113238999 residues
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                                                                                                  December 19, 2001, 18:34:13
                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      using sw model
                                                                                                                                                                                                                      IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                                                     US-09-485-529-105
51
                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0 Maximum DB seq length: 20000000000
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Match Length DB
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1100 3
4403765
4411529
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                                                                                                                                                                                          Sequence:
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                                                                                                                                                             Title:
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Sequence 3, Appli
Sequence 1, Appli
Sequence 23, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 17, Appl
Patent No. 5229279
Patent No. 5512669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                 5512669-5
US-08-743-637B-20
US-08-526-840B-20
US-08-748-170A-3
US-09-047-148-1
                                                                                   US-08-241-943-23
US-08-254-357-1
US-09-061-702-3
US-09-046-992-1
US-08-510-646B-17
5229279-5
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS PRICE
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELEPHONE: (202 638-6666
TELEPHONE: (202) 39305350
TELEPHONE: (202) 39305350
TELEPHONE: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 16:
                                                US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-006-676B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-428-414A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encor
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/09385028
Patent No. 6232106
GENERAL INFORMATION:
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COUNTY: U.S.A.
21P: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: DNA (genomic)
US-09-385-028-16
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Length 1542;

4;

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GENERAL INFORMATION:
APPLICANT: Harberd, Nicholas P
APPLICANT: Pend, Jinrong
APPLICANT: Carol, Pierre
APPLICANT: Richards, Donald E
APPLICANT: Richards, Donald E
FILE PEFERENCE: 620-45
                        DNA Sequence Encoding Enzymes of Clavulanic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 15079;
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                                                                                       NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452USZ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 29.8; DB Pred. No. 0.24;
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CURRENT FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: PCT/GB97/00390
EARLIER FILING DATE: 1997-02-12
EARLIER APPLICATION NUMBER: GB 9602796.6
EARLIER FILING DATE: 1996-02-12
                                                                   Acid Biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ), ORGANISM: Streptomyces clavuligerus US-09-385-028-1
                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09117853
Patent No. 6307126
      Ashish S. Paradkar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202 638-6666
TELEFAX: (202) 39305350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
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75.5%;
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.5
Matches 37; Conservative
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                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NOS: 12
                        TITLE OF INVENTION: Patent No. 6232106 TITLE OF INVENTION:
                                                                                                                                                                              Washington
                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                              CITY: Wash:
STATE: D.C
                                                                                                                                                                                                                       COUNTRY: U
      APPLICANT:
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US-09-117-853-1
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                             Gaps
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APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Blosynthesis
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                                                                                           909 CGAGCTGCTGCCGCAGCTCCCGTACGCGTGTGGGCCTCCGAGTCGGTG 957
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                          12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                     cgagctgctggcggcgctcgggtacaaggtgcgcgctccgacatggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                              JACOBSON, PRICE, HOLMAN & STERN, PPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-666
TELEFANCE: (202) 39305350
TELETER: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 13:
    Pred. No. 0.23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.4%; Score 29.8; Dilarity 75.5%; Pred. No. 0.24 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                                                         Sequence 13, Application US/09385028 Patent No. 6232106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09385028
Patent No. 6232106
GENERAL INFORMATION
APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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1 Similarity 75.5%;
37; Conservative (
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LENGTH: 11604 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
  Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                   US-09-385-028-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-385-028-13
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                                                                                                                                                                              RESULT
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Gaps

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Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 69.4%;
Matches 34; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 69.4%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
LENGTH: 4411529
                                                                                                         US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 773;
                                                                                                                        51.0%; Score 26; DB 4; Length 1964; 70.0%; Pred. No. 3.5; Live 0; Mismatches 15; Indels
                                                                                                                                                                                                                  1 gacgagetgetggeggegetegggtacaaggtgegegeetegacatgge 50
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: C1-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER FILING DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SOFTHARE: Microsoft Word Version 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25.8;
Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER FILING DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 39
LENGTH: 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-09-248-335-53
; Sequence 53, Application US/09248335
; Patent No. 6096504
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                      Sequence 39, Application US/09248335 Patent No. 6096504
                                 TYPE: DNA
CORGANISM: Arabidopsis thaliana
US-09-117-853-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.68;
73.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 50.6%;
1 Similarity 73.3%;
33; Conservative
                                                                                                                                          Best_Local Similarity 70.0
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: maize US-09-248-335-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: maize US-09-248-335-53
SEQ ID NO 1
LENGTH: 1964
                                                                                                                                                                                                                                                                                     RESULT 5
US-09-248-335-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PUBBRCHOIN: TUBERCHOOSIS
FITLE OF INVENTION: TUBERCHOOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FASSEN, Claire M.
APPLICANT: FASSEN, Claire M.
APPLICANT: USENGER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERBNCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
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Pred. No. 7.4;
0; Mismatches 15; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 4; Length 4403765;
Pred. No. 7.4;
0; Mismatches 15; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis
CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mycobacterium tuberculosis FEATURE:
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TITLE OF INVENTION: CARBAMOYL-PHOSPHATE SYNTHETASE GENE OF CORVNEFORM TITLE OF INVENTION: BACTERIA AND METHOD FOR PRODUCING L-ARGININE FILE REPERDER: 09945CIP
CURRENT APPLICATION NUMBER: US/09/629,616
CURRENT FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 4837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Granneman, James G.
APPLICANT: Lahners, Kristine N.
APPLICANT: Lahners, Kristine N.
APPLICANT: Lahners, Kristine N.
APPLICANT: Ran, Donald D.
TITLE OF INVENTION: @ @3-ADRENBERIC RECEPTOR PROTEIN AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &
ADDRESSEE: MILTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 4837;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24.4; DB 4; Length 4 Pred. No. 11; 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390 CITY: TOY STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 cgagctgctggcggcgctcgggtacaaggtgcgcgctccga
                                                                                                                                                                                                               TYPE: DNA ORGANISM: Brevibacterium lactofermentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Paint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SURENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,901
FTI.ING DATE: 19920220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19920720
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOIN, Kenneth I.
REGISTRATION NUMBER: 30,955
REFREDENCE/DOCKET NUMBER: P-32.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-916-901-5/c
; Sequence 5. Application US/07916901
; Patent No. 5364772
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 47.8%;
Best Local Similarity 73.8%;
Matches 31; Conservative
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LENGTH: 2005 base pairs
                                                                                                                                                                                                                                                       ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (283)..(1461)
; NAME/KEY: CDS
; LOCATION: (1470)..(4808)
US-09-629-616-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: NUCLEIC ACID STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                   APPLICANT: Philippsen, Peter
APPLICANT: Poliman, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Wondrand, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Reclassing, Corinne
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 AGGACCTGATGCCGTCGCTGGAGAGATGCACGTCTCGTCCATTGCG 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.8%; Score 24.4; DB 68.0%; Pred. No. 11; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                   Sequence 401, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-629-616-1
; Sequence 1, Application US/09629616
; Patent No. 6255086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF,
TELECOMMUNICATION: TELECOMMUNICATION: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 401: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HASHIGUCHI, Kenichi
NAKAMATSU, Tsuyoshi
KURAHASHI, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 68.0
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KUWABARA, Yoko
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MORI, Yukiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAG1300UP
                                                                                                   GENERAL INFORMATION:
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                                 JS-08-998-416-401
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OTHER INFORMATION: "n" bases at various positions throughout the sequence

OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
UNMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2.2
                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 1568431 GATGTGCTGGTGCTGCGCTTCAAGGTGCTAGACACCGACA 1568386
                                                                 Score 24; DB 1; Length 2005; Pred. No. 14;
                                                                                                                   Indels
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APPLICANT: EVANS, RONALD M.
APPLICANT: MANGELSDORF, DAVID J.
TITLE OF INVENTION: RETINOID RECEPTOR COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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STREET: 444 SOUTH FLOWER STREET, SUITE 2000
CITY: LOS ANGELES
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PAPPLICATION DATA:
APPLICATION NUMBER: US/08/336,408B
FILING DATE: 08-NOV-1994
                                                                                                                                                               6 gctgctggcggcgctcgggtacaaggtgcgcgcctccgac 45
                                                                                                                                                                                         131 GETGTTGGCTGCACTGGGGTCCAAGGTGGGGGGCGTCTGAC 92
                                                                                                                 0; Mismatches
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TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09103840A Patent No. 6294328
                                                                   47.1%;
75.0%;
                                                                 Query Match
Best Local Similarity 75.0
Matches 30; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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USA
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US-08-336-408B-1
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US-07-916-901-5
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GENERAL INFORMATION:
APPLICANT: Mangelsdorf, Dr., David J.
APPLICANT: Bangelsdorf, Dr., David J.
TITLE OF INVENTION: RETINOID RECEPTOR COMPOSITIONS AND TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00399
FILING DATE: 19910122
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/478,071
FILING DATE: 09-FEB11990
ATTORNEY/AGENT INFORMATION:
NAME: RELEAT, Mr., Stephen E.
REGISTRATION NUMBER: 31192
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STREET: 135 South LaSalle Street, Suite 900
CITY: Chicago
CITY: Illinois
COUNTRY: USA
ZIP: 60603
PULGATION DATA:
APPLICATION NUMBER: US 07/933,453
FILING DATE: 11-AUG-1992
PRILING DATE: 12-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US91/00399
FILING DATE: 22-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US91/00399
FILING DATE: 09-FEB-1990
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,192
REFRERENCE/DOKER UNMBER: 31,192
RECISTRATION NUMBER: 31,192
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 50852
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (619) 552-1313
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76..1464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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US-08-336-408B-1
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PCT-US91-00399-1
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APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 44.7%; Score 22.8; DB 1; Length 1 Best Local Similarity 66.0%; Pred. No. 34; Matches 33; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSTLVANIA AVE. N.W.
CITY: WASSINGTON
STATE: D.C.
COUNTRY: USA
2.1P: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION NUMBER: 36,217
REGISTRATION NUMBER: 36,217
REGISTRATION NUMBER: 36,217
RELECOMMULICATION INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
RELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEFRAX: (202) 887-1517
THENTEY. (202) 887-1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23.4; DB 5;
Pred. No. 22;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08440856A Patent No. 5750873
TELEFAX: (619) 552-0095
TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1866 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: 1inear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: RXR HUMAN ALPHA
FERFIRE:
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1236 base pairs
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Best Local Similarity 67.3%;
Matches 33; Conservative
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join(76..1464)
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STRANDEDNESS: single
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; LOCATION:
PCT-US91-00399-1
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US-08-440-856A-1
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DB 1; Length 1236;

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Search completed: December 19, 2001, 21:44:58 Job time: 11445 sec
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Page 7

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-Q-/cgn2_1/USPTO_spool/USO9485529/runat_19122001_165005_14373/app_query.fasta_1.77
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-THR_MAX-100 -THR_MIN-0 -ALIGN-50 -MODE-LOCAL -OUTFMT-pfs
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-USER-US09485529_@CGGN1_1_248 -NCPU-6 -ICPU-3 -LONGLOG -NO_XLPXY
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                                                                                                        Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
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\$1002,/gcgdata/geneseq/geneseq/NA2000_DAT.AAC99128 + \$1002,/gcgdata/geneseq/geneseq/NA2000_DAT.AAC99088 + \$1002,/gcgdata/geneseq/geneseq/NA2000_DAT.AAC99088 + \$1002,/gcgdata/geneseq/geneseq/NA2000_DAT.AAC99088 + \$1002,/gcgdata/geneseq/geneseq/NA2000_DAT.AAC99098 + \$1002,/gcgdata/geneseq/geneseq/NA2000_DAT.AAC9909 + \$1002,/gcgdata/geneseq/geneseq/NA2000_DAT.AAC9307 + \$1002,/gcgdata/geneseq/geneseq/geneseq/NA2000_DAT.AAC9307 + \$1002
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6623317 663337 7463330 7463330 7463330 7463330 7463330 7463330 74630 746330 746	1150 1150 1150 1150 1155 1158 1158 1173 1173 1184 1184
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333.00 333.00	000000000000000000000000000000000000000

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Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence obtained after sequencing wheat Rht clone 14al.
                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36263
                                                         to: AAX36284 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PLAN-) PLANT BIOSCIENCE LTD.
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                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAX36263 standard; DNA; 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97GB-0017192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUL-1999 (first entry)
            US-09-485-529-104 x AAX36284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-181040/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09909174-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
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                                                            Align seg 1/1
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513445
1664976
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585
603
807
851
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1.5e+06
1.7e+06
1.9e+06
1.9e+06
591.93
691.86
                                                                                                                                                                       1.2e+03
1.2e+03
1.7e+03
1.9e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene; homologue; Triticum aestivum; wheat; growth inhibition; gonist; glbberellin; dwarf phenotype; glbberellin blosynthesis;
          41.61
37.81
26.18
25.24
108.27
107.05
104.83
103.01
102.71
99.83
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          33.00
33.00
33.00
33.00
32.50
32.50
32.50
32.50
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Percent Identity: 100.000
                           /SIDS2/gcgdata/geneseq/geneseqn/MA2001.Darr.AAIG1373-
/SIDS2/gcgdata/geneseq/geneseqn/NA198.Darr.AAIG1373-
/SIDS2/gcgdata/geneseq/geneseqn/NA199.Darr.AAI42209-
/SIDS2/gcgdata/geneseq/geneseqn/NA2001.Darr.AAI42830+
/SIDS2/gcgdata/geneseq/geneseqn/NA2001.Darr.AAI42830+
/SIDS2/gcgdata/geneseq/geneseqn/NA2001.Darr.AAI4205+
/SIDS2/gcgdata/geneseq/geneseqn/NA1097.Darr.AAI42204+
/SIDS2/gcgdata/geneseq/geneseqn/NA2000.Darr.AAI42204+
/SIDS2/gcgdata/geneseq/geneseqn/NA2000.Darr.AAI42204+
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/SIDS2/gcgdata/geneseqn/NA2000.Darr.AAI42204+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide derived from the wheat rht gene.
            /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH68530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harberd NP, Peng J, Richards DE;
                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:

XX
AAX36284;
XX
AAX36284;
XX
T16-JUL-1999 (first entry)
XX
Oligonuclectide derived from the
XX
WR th gene; homologue; Triticum ae;
XX
WR th gene; homologue; Triticum ae;
XX
XX
Triticum aestivum.
XX
XX
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Triticum aestivum.
XX
XX
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YI
3-AUG-1999; 98WO-GB02383.
XX
XX
XX
(PLAN-) PLANT BIOSCIENCE LTD.
XX
XX
Claim 3; Page 53; 88pp; English.
XX
XX
Claim 3; Page 53; 88pp; English.
XX
Claim 3; Page 53; 88pp; English.
XX
Claim 3; Page 53; 8dpp; English.
XX
Claim 3; Page 54; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 53; 88pp; English.
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Ratio: 4.765
Percent Similarity: 100.000
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its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by globerallin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin blosynthesis, such as paclobutazol, e.g. to allow use of a gibberellin blosynthesis inhibitor to keep weeds obtained after partially commenced.
                                                                                                The specification describes polypeptides encoded by the Rht gene (and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                obtained after partially sequencing wheat Rht clone 14al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 453 BP; 85 A; 136 C; 158 G; 67 T; 7 other
Disclosure; Fig 2b(9); 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 81.00
Ratio: 4.765
Percent Similarity: 100.000
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alignment_block:

which is

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Thu Dec

to: 453

from: 1

to: AAX36263

Align seg 1/1

US-09-485-529-104 x AAX36263

Wheat Rht clone 5al genomic sequence

paclobutrazol; ss. Friticum aestivum.

WO9909174-A1

16-JUL-1999 (first entry)

AAX36279;

ВP

seq_documentation_block:
ID AAX36279 standard; DNA; 2125

323 G 323

17 a 17

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin.insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence represents the wheat Rht clone 5al genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Triticum Aestivum polynucleotides · encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2125 BP; 325 A; 768 C; 723 G; 309 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 17
Gaps: 0
Percent Identity: 100.000
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Ratio: 4.765
Percent Similarity: 100.000
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P-PSDB; AAY02540.
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Assituum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the composite DNA sequence of wheat Rht gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                             omologue; Triticum aestivum; wheat; growth inhibition; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2709 BP; 473 A; 900 C; 823 G; 482 T; 31 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 17
Gaps: 0
Percent Identity: 100.000
                                                    to: 2125
                                                                                                                                                                                                                                                                                                                                                                                                            Composite DNA sequence of wheat Rht gene.
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                                                    from: 1
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Ratio: 4.765
Percent Similarity: 100.000
               US-09-485-529-104 x AAX36279
                                                    to: AAX36279
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Rht gene; homologue;
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                                                                                                                                                                                                                                                                            seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       paclobutrazol; ss
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alignment_block
                                                    Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                    AAX36275;
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                                                                                                                                                                                                                                                                                                                                    Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                   seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36279
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DE;

Richards

Harberd NP, Peng J,

(PLAN-) PLANT BIOSCIENCE LTD

98WO-GB02383, 97GB-0017192,

07-AUG-1998; 13-AUG-1997;

25-FEB-1999

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Assituum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by the conferring a dwarf phenotype on a plant which is correctable used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin blosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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                                                                                                                                                                                  seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36281
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                                                                                                            to: 2709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Partial sequence of the maize D8-1 allele.
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                                                                                                            from: 1
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                                  US-09-485-529-104 x AAX36275
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                                                                                                            to: AAX36275
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P-PSDB; AAY02542.
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                323 G 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX36281;
                                                                                                                                                                                                                                                                                                                                          17 a 17
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by growth of the plant. This growth inhibition is antagonised by growth of the plant. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with any be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin blosynthesis, such as paclobutrazol, compounds which inhibit gibberellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the partial sequence of the maize D8-2023 allele.
                                                                                                                                                                                                                                                                                                                                                                                                                          Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; maize; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                      100 GATGAGCTGCTGGCGCTCGGGTACAAGGTGCGTTCGTCGAAATGGC 149
                                                                                   1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36282
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                                                                                                                                                                                                                                                                                                                                                                                           Partial sequence of the maize D8-2023 allele.
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Gaps:
                                                to: 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Richards DE;
                                                to: AAX36281 from: 1
                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                seq_documentation_block:
ID AAX36282 standard; DNA; 371
                                                                                                                                                                                                                                                                                                                                                         16-JUL-1999 (first entry)
alignment_block:
US-09-485-529-104 x AAX36281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-181040/15.
P-PSDB; AAY02543.
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                                                Align seg 1/1
                                                                                                                                                                                             150 G 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays.
                                                                                                                                                          a 17
                                                                                                                                                                                                                                                                                                                        AAX36282;
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Ratio:

Length: 17 Gaps: 0 Percent Identity: 94.118

Quality: 78.00 Ratio: 4.588 Percent Similarity: 100.000

alignment_scores:

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth inhibition is antagonised by globerellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with globerellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being globerellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit globerellin blosynthesis, such as paclobutrazol, e.g. to allow use of a globerellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; rice; expressed sequence tag; EST; ss.
                                                                                                                   seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36277
                                                                                                                                                                                                                                                                                                                                                                                                                     Rice EST D39460 sequence, homologous to wheat Rht gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 770 BP; 104 A; 252 C; 294 G; 120 T; 0 other;
 Percent Identity: 94.118
                                                                                    to: 371
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                                                                                                                                                                                                                                                                                         from: 1
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                                alignment_block:
US-09-485-529-104 x AAX36282
                                                                                  to: AAX36282
Percent Similarity: 100.000
                                                                                    Align seg 1/1
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alignment_scores:

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its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence represents the maize lal genomic clone sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Triticum Aestivum polynucleotides · encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homologue; Triticum aestivum; wheat; growth inhibition; ;; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36280
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 Length: 17
Gaps: 0
Percent Identity: 94.118
                                                                                                                        to: 770
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                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize lal genomic clone sequence.
                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID AAX36280 standard; DNA; 2255 BP.
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                                                                      alignment_block:
US-09-485-529-104 x AAX36277
                                                                                                                      to: AAX36277
Quality: 78.00
Ratio: 4.588
Percent Similarity: 100.000
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                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene;
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by globerellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Tailer plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin blosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the partial cDNA sequence of rice AAD39460 (a wheat Rht gene homologue)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Partial cDNA sequence of rice D39460 (a wheat Rht gene homologue).
                                                                                                                                                                                                           1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36276
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               Length: 17
Gaps: 0
Percent Identity: 94.118
                                                                                                                                                    to: 2255
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AAX36276 standard; DNA; 725 BP
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                                                                                        alignment_block:
US-09-485-529-104 x AAX36280
             Quality: 78.00
Ratio: 4.588
Percent Similarity: 100.000
                                                                                                                                                  Align seg 1/1 to: AAX36280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antagonist; gibber
paclobutrazol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa
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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX36276;
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Asstivum, inhibit growth of the plant. This growth inhibition is antagonised by glubberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gluberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gluberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologus gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gluberellin blosynthesis, such as paclobutrazol, eg. to allow use of a gluberellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was obtained after partially sequencing wheat Rht clone 5al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence obtained after sequencing wheat Rht clone 5al.
                                                                                                                                                                                                                                                                                                                                                                                                               109 GAGCTGCTGGCGCGCTCGGGTACAAGGTGCGGTCGTCCGACATGGCC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36273
                                                                                                                                                                                                                                                                                                                                                                        2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
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Gaps: 0
Percent Identity: 100.000
                           Length: 16
Gaps: 0
Percent Identity: 93.750
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                                                                                                                                                                                                                                                                                                  to:
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ID AAX36273 standard; DNA; 324 BP.
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US-09-485-529-104 x AAX36276
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Percent Similarity: 100.000
                                                                 Ratio: 4.500
Percent Similarity: 100.000
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Ratio:
                                  Quality:
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alignment_scores
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alignment_block:
US-09-485-529-104 x AAC65312
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-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                   306 T 306
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SCARECROW-like (SCL) genes encoding proteins containing an amino acid sequence similar to the sequence of MOTIF III (VHIID) of Arabidopsis SCR protein are disclosed. SCR and SCL genes are useful for producing transgenic plants whose cell division is modified and root and/or stem development and gravitropism of stem or hypocotyl is altered. Cell division is increased or decreased in roots resulting in thicker or thinner root development. The transgenic plants are useful for expressing a gene of interest encoding a gene product that confers herbicide, salt, pathogen or insect resistence in root or embryos and genes encoding starch, lighth or cellulose biosynthesis in shoots. The SCR gene also confers less susceptibility to lodging in the transgenic plants than a wild-type plant. SCR gene sequences are also useful as molecular markers in the sequences are also useful as molecular markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scarecrow gene; SCR gene; plant; regulatory gene; SCARECROW-like; SCL; transgenic plant; cell division; molecular marker; herbicide resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scarecrow gene useful for producing transgenic plants expressing genes whose product increases starch, lignin or cellulose biosynthesis and confers herbicide, pathogen or insect resistance
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                                                                                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC65312
                                                                                                                                                                    Align seg 1/1 to reverse of: AAX36273 from: 1 to: 324
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Helariutta Y, Bruce W, Lim J;
                                                     US-09-485-529-104 x AAX36273/rev
                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID AAC65312 standard; cDNA; 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis SCL EST T22782.
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Ratio: 4.118
Percent Similarity: 100.000
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                            alignment_block:
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HANDER PRODUCTION OF THE PRODUCT OF

Percent Identity: 82.353

Gaps:

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                         1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC45745
                                                                                                                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 47609.
to: 457
from: 1
                                                                                               seq_documentation_block:
ID AAC45745 standard; DNA; 1602
                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0132485.
99US-0132486.
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99US-0134218.
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99US-0137528
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                                                                                                                                       18-OCT-2000 (first entry)
Align seg 1/1 to: AAC65312
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	Length:
PR 06-AUG-1999; 99US-0147413. PR 10-AUG-1999; 99US-0147413. PR 11-AUG-1999; 99US-0147433. PR 11-AUG-1999; 99US-0148171. PR 11-AUG-1999; 99US-0148171. PR 11-AUG-1999; 99US-0148171. PR 12-AUG-1999; 99US-0148171. PR 20-AUG-1999; 99US-0148171. PR 20-AUG-1999; 99US-0148171. PR 20-AUG-1999; 99US-014972. PR 21-AUG-1999; 99US-014972. PR 22-AUG-1999; 99US-014972. PR 22-AUG-1999; 99US-014972. PR 23-AUG-1999; 99US-014972. PR 23-AUG-1999; 99US-014972. PR 23-AUG-1999; 99US-011992. PR 23-AUG-1999; 99US-011992. PR 23-AUG-1999; 99US-011992. PR 23-AUG-1999; 99US-011993. PR 23-AUG-1999; 99US-011992. PR 23-AUG-1999; 99US-011993. PR 23-AUG-1999; 99US-011993. PR 23-AUG-1999; 99US-011993. PR 23-AUG-1999; 99US-011993. PR 24-AUG-1999; 99US-011993. PR 24-AUG-1999; 99US-011993. PR 24-SEP-1999; 99US-011993. PR 24-CCT-1999; 99US-011993. PR 24-CCT-1999; 99US-011993. PR 24-CCT-1999; 99US-011993. PR 21-CCT-1999; 99US-011993. PR 21-CCT-1999; 99US-011993. PR 22-CCT-1999; 99US-011993. PR 23-CCT-1999; 99US-011993	alignment_scores: Quality: 70.00
990CS - 0137502 990CS - 0137724 990CS - 0138640. 990CS - 0138640. 990CS - 0139119. 990CS - 0139119. 990CS - 0139452. 990CS - 0139452. 990CS - 0139452. 990CS - 0139456. 990CS - 0139456. 990CS - 0139461. 990CS - 014085. 990CS - 014085. 990CS - 014085. 990CS - 014085. 990CS - 014085. 990CS - 0144631. 990CS - 0144632. 990CS - 0145088. 990CS - 0145088.	908-014 908-014
28	05-AUG-199
PR P	

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creators which may be used to modify phenotype associated with a plant's sugar sensing characteristics and increasing yield when their expression level is altered. Sugars are central regulatory molecules that control superts of physiology, metabolism and development. Therefore the cDNAs and proteins of the invention are useful for modifying the growth and germination rates of plants, photosynthesis, glyoxylate metabolism, response, wounding response, cell cycle regulation, pathogen response, wounding response, cell cycle regulation, pathogen response, wounding response, cell cycle regulation, pagmentation, flowering and senescence of plants and for modifying sink source relationships in seeds, tubers, roots, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and polypeptides may be used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peepers, pineapple, spineaple, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription factor; biochemical characteristic; controlling element; structural characteristic; developmental characteristic; gene therapy; agricultural biotechnology; plant trait modification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/genesegn/NA2001.DAT:AAD05776
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                                                                                                                                                                                                                                                                                                                                                 other;
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Gaps: 0
Percent Identity: 82.353
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1.1764
/*tag= a
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ID AAD05776 standard; cDNA; 1764 BP
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17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
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US-09-485-529-104 x AAD06661
                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio: 4.118
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant transcription factor; phenotype; sugar sensing characteristic; transgenic plant; plant yield; growth; germination; photosynthesis; glyoxylate metabolism; respiration; pathogen response; wounding response; cell cycle regulation; planentation; flowering; senescence; physiology; storage organ; metabolism; sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides, useful plants and increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent relates to polynucleotides encoding 35 plant transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JL;
                                                                                                                                                     1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                              A. thaliana transcription factor G308 homolog, G307 cDNA.
                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseg/genesegn/NA2001.DAT:AAD06661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product- "Transcription factor homolog"
        Gaps: 0
Percent Identity: 82.353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yield, e.g. corn, potato and cotton plants -
                                                                                                    to: 1602
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1..1764
                                                                                                    from: 1
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ID AAD06661 standard; cDNA; 1764 BP.
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17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
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                                                                                                                                                                                                                                                                                                                                                                              10-AUG-2001 (first entry)
                                                    alignment_block:
US-09-485-529-104 x AAC45745
                                                                                                    Align seg 1/1 to: AAC45745
      Ratio: 4.118
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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PILGRIM M.
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(RIEC/)
(YUGG/)
(SAMA/)
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(HEAR/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
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The present sequence is Arabidopsis thaliana transcription factor, G307 cDNA. The transcription factor is used for altering a plant's biochemical characteristics. The transcription factor may be used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugar cane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, egyplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers, plneaple, splnach, squash, sweet corn, tobacco, tomato, watermelon, cosaceous fuuts and/or vegetable brassicas. Transcription factors are key controlling elements of biological pathways and altering expression levels of 1 or more transcription factors can change entire biological pathways in an organism. Therefore manipulating transcription factor fevels in plants offers great potential in agricultural biotechnology for modifying a plant's traits. Transcription factor cDNA is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding plant transcription factor polypeptides, useful for altering the biochemical characteristics of plants e.g. corn,
                                                                                                                                                                                                                                                                                                                                                                                                         Samaha R;
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C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0
Percent Identity: 82.353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 66-68; 127pp; English.
                               MENDEL BIOTECHNOLOGY INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Jiang
                                                                                                                                                                                                                                                                                                                                                                                                         Adam L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               octato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-AUG-2001 (first entry)
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Percent Similarity: 100.000
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                                                              CREELMAN R.
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                                                                                                                                                                                               HEARD J.
SAMAHA R.
PILGRIM M.
PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAE01892
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                                                                                                                                ADAM L.
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                                                                                                                                                                                                                                                                     (PILG/)
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                                  MEND-)
                                                              CREE/)
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NAME OF THE PROPERTY OF THE PR
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The patent relates to polynucleotides encoding 35 plant transcription factors which may be used to modify phenotype associated with a plant's sugar sensing characteristics and increasing yield when their expression level is altered. Sugars are central regulatory molecules that control aspects of physiology, metabolism and development. Therefore the CDNAs and proteins of the invention are useful for modifying the growth and germination rates of plants, photosynthesis, glyoxylate metabolism, respiration, starch and sucrose synthesis and degradation, pathogen response, wounding response, cell cycle regulation, plydmentation, plowering and senescence of plants and for modifying sink-source relationships in seeds, tubers, roots, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and polypeptides may be used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, collee, cucumber, eggplant, grapes, honey dew, lettuce, mango, meton, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, meton, onlon, papaya, peas, peppers, pleapple, spinach, squash, sweet con,
Plant transcription factor; phenotype; sugar sensing characteristic; transgenic plant, plant yield; growth; germination; photosynthesis; glyoxylate metabolism; respiration; pathogen response; wounding response; cell cycle regulation; pigmentation; flowering; senescence; physiology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas present sequence is an Arabidopsis thallana transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding plant transcription factor polypeptides, useful for altering the sugar sensing characteristics of plants and increasing yield, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riechmann JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1951 BP; 482 A; 419 C; 475 G; 575 T; 0 other;
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                                                                                                                                                                            /*tag= a
/product= "Transcription factor"
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                                                                                                                                         Location/Qualifiers
196..1794
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                                                                    storage organ; metabolism; ss
                                                                                                                                                                                                                                                                                              14-NOV-2000; 2000WO-US31414
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2000US-0227439
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4.118
                                                                                                     Arabidopsis thaliana.
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YU G.
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P-PSDB; AAE02545.
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Yu G, Samaha R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PINEDA O.
PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                        JIANG C.
HEARD J.
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                                                                                                                                                                                                                               W0200135725-A1
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22-AUG-2000;
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                                                                                                                                                                                                                                                                 25-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                    (JIAN/)
(HEAR/)
(PINE/)
(PILG/)
(ADAM/)
(RIEC/)
                                                                                                                                                                                                                                                                                                                                                                                                       (MEND-)
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                                                                                                                                         Key
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324 T 324

17 a 17

AAD05791;

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such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugar cane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, onlon, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. Transcription factors are key controlling elements of biological pathways and altering expression levels of 1 or more transcription factors can change entire biological pathways in an organism. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biology for modifying a plant's traits. Transcription factor cDNA is need.
  alter the structure and developmental characteristics of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding gibberellin inhibitor GAI and related antisense sequences – used to create tall, or particularly, dwarf plants, especially crops such as maize, rice and wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gibberellin insensitivity, gai; plant growth inhibition, dwarf phenotype; lodging resistance; increased yield; flowering regulation; bolting inhibition; spinach; lettuce; antibody; identification; probe; primer; antisense; sense; expression regulation; co-suppression; rice; Bakane disease resistance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT91937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana gibberellin insensitivty gene gai.
                                                                                                                                                                                                                                                                                             Sequence 1951 BP; 482 A; 419 C; 475 G; 575 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                             Length: 17
Gaps: 0
Percent Identity: 82.353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peng J, Richards DE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                       is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-485-529-104 x AAD05791
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT91937;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is Arabidopsis thaliana transcription factor, G308 cDNA, a homologue of G307. The transcription factor is used for altering a plant's biochemical characteristics. The transcription factor may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription factor; biochemical characteristic; controlling element; structural characteristic; developmental characteristic; gene therapy; agricultural biotechnology; plant trait modification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding plant transcription factor polypeptides, useful for altering the biochemical characteristics of plants e.g. corn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Samaha R;
                                                                                                                                                                     274 GATGAGCTTCTAGCTGTTCTTGGTTACAAGGTTAGGTCATCGGAAATGGC 323
                                                                                                                                                1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAD05791
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C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana transcription factor, G308 cDNA.
    Percent Identity: 82,353
                                                                                                       to: 1951
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196..1794
/*tag= a
                                                                                                       from: 1
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                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID AAD05791 standard; cDNA; 1951 BP
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O, Jiang
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22-AUG-2000; 2000US-0227439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2001 (first entry)
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                                      alignment_block:
US-09-485-529-104 x AAD06646
                                                                                                     to: AAD06646
Percent Similarity: 100.000
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ADAM L.
RIECHMANN J L.
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SAMAHA R.
PILGRIM M.
PINEDA O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200136597-A1
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                                                                                                       Align seg 1/1
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Key

(RIEC/) (HEAR/) (SAMA/) (PILG/) (PINE/)

(JIAN/)

(ADAM/)

CREE/) (XDGG/)

Tanguy X;

Froger N,

Barret P, Brunel D,

Delourme R,

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(INRG ) INRA INST NAT RECH AGRONOMIQUE.
Renard M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HANDER STATE OF STATE
GRAS protein; BZH gene; transcription factor; gibberellin; morphogenesis; plant development; dwarf plant; crucifer; ss.
                                                                                                                                          insensitivity (gai) gene product (GAI), the expression of which inhibits plant growth. However the inhibition is antagonised by combined that is insensitivity (gai) expression confers a dwarf phenotype that is insensitive CGA, while gai expression confers a dwarf phenotype produce tall or dwarf plants, particularly the latter for increased resistance to lodging and increased yield. It may also allow regulation of flowering, i.e. plants remain in the vegetative state until treated with GA, useful to inhibit boilting in spinach and letture. GAI can be used to raise specific antibodies for identifying homologous proteins or genes in other species. gai fragments can also be used as probes or primers to identify and sense expression regulating (co-suppressing) sequences. Rice plants that express GAI may be resistant to Bakane disease. Mainfulation of gai and GAI makes it possible to tailor the degree of dwarfism
                                                                                                             The present sequence encodes the Arabidopsis thaliana gibberellin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF25480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and GA sensitivity to particular crops or situations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 0
Percent Identity: 82.353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of a wildtype GRAS protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
60..1778
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "GRAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:

XX
AC AAF25480;
XX
XY
XX
T 15-MAY-2001 (first entry)
XX
XX
XX
Nucleotide sequence of a wildty;
XX
KW
GRAS protein; BZH gene; transcr.
XX
SBrassica napus.
XX
XX
NX
SFT
CDS
XX
XX
NO200109356-A1.
XX
PD
OB-FEB-2001.
XX
PD
OB-FEB-2001.
XX
PD
XX
PR
CO2-AUG-1999; 99FR-0010023.
XX
XX
PR

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                                        Claim 2; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouality: 70.00
Ratio: 4.118
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-485-529-104 x AAT91937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAT91937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 T 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 a 17
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GRAS protein; BZH gene; transcription factor; gibberellin; morphogeneals; plant development; dwarf plant; crucifer; ss.
                                                                                                                                                                                             The present sequence encodes a wild type plant protein of the GRAS family. The specification describes a mutant allele of the BZH gene, which contains a f1655A mutation resulting in the mutation E546K in the protein. GRAS proteins are transcription factors implicated in regulation of the response to gibberellins and thus in control of morphogenesis and plant development. The mutant GRAS protein is used to produce dwarf plants, specifically cruoifers. Dwarf plants be sown earlier (increasing nitrate accumulation without risking excessive stem growth during winter), and have better resistance to cold and lodging. They are also easier to harvest and allow for better monitoring of the crop.
                                                                              Ç
                                                                   New mutant nucleic acid encoding modified GRAS family protein, used produce dwarf transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF25481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1779 BP; 418 A; 430 C; 476 G; 455 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 17
Gaps: 0
Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of a mutant GRAS protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1779
                                                                                                                                                          Example 1; Page 13-15; 28pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
60..1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: AAF25480 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "GRAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID AAF25481 standard; DNA; 1779 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-2000; 2000WO-FR02216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99FR-0010023
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-485-529-104 x AAF25480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 3.882
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.00
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WPI; 2001-182964/18
                           P-PSDB; AAB31883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica napus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 T 233
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AAX36283 standard; DNA; 416 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97GB-0017192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                        4.643
93.333
                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-485-529-104 x AAX36266
                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAX36266
                                                                                                                                                                                                                                                                                             65.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harberd NP, Peng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rht gene; homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-181040/15.
P-PSDB; AAY02544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          paclobutrazol; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum
                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9909174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1997;
                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX36283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a mutant plant protein of the GRAS family. The mutant allele of the BZH gene contains a G1695A mutation resulting in the mutation E546K in the protein. GRAS proteins are transcription factors implicated in regulation of the response to gibberellins and thus in control of morphogenesis and plant development. The mutant GRAS protein is used to produce dwarf plants, specifically crucifiers. Dwarf plants may be sown earlier (increasing nitrate accumulation without risking excessive stem growth during winter), and have better resistance to cold and lodging. They are also easier to harvest and allow for better monitoring of the crop.
                                                                  ţ
                                                                 encoding modified GRAS family protein, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
           Tanguy X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence obtained after sequencing wheat Rht clone 14al.
                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36266
           Froger N,
                                                                                                                                                                                                                                                Sequence 1779 BP; 419 A; 430 C; 475 G; 455 T; 0 other;
                                                                                                                                                                                                                                                                                           Length: 17
Gaps: 0
Percent Identity: 76.471
           Brunel D,
                                                                                                                                                                                                                                                                                                                                                                         to: 1779
                                                                                                  Example 1; Page 18-20; 28pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Richards DE;
          Barret P,
                                                                                                                                                                                                                                                                                                                                                                        to: AAF25481 from: 1
                                                                             produce dwarf transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PLAN-) PLANT BIOSCIENCE LTD
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                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-485-529-104 x AAF25481
                                                                                                                                                                                                                                                                                           Quality: 66.00
Ratio: 3.882
Percent Similarity: 100.000
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ID AAX36266 standard; DNA;
                                                                 New mutant nucleic acid
           Delourme R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harberd NP, Peng J,
                               WPI; 2001-182964/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-181040/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     paclobutrazol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum.
                                           P-PSDB; AAB31884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9909174-A1
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                                                                                                                                                                                                                                                                                  alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1
         Renard M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 T 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX36266;
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants can be be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as pacloburrazol, eg. to allow use of a gibberellin biosynthesis, such as pacloburrazol, dwarf but let crop plants grow tall. The present sequence was dwarf with eartially sequencing wheat Rht clone 14al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is
New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mologue; Triticum aestivum; wheat; growth inhibition;
gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 GACTATCTGCTGGCGGCGCTCGGGTACAAGGTGCGCGCCTCCGAC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 200 BP; 24 A; 58 C; 84 G; 27 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Partial sequence of the wheat rht-10 allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 200
                                                                                                                                                                                                                Disclosure; Fig 2b(12); 88pp; English.
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plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as pacibutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the partial sequence of the wheat rht-10 allele.
                                              The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit prowth of the plant. This growth inhibition is antagonised by globberellin. The products can be used to provide Rht expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence obtained after sequencing wheat Rht clone 14al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seg_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36261
                                                                                                                                                                                                                                                                                               Length: 13
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                             Sequence 416 BP; 59 A; 168 C; 129 G; 60 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                 5 AlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCGGCGCTCGGGTACAAGGTGCGCGCCTCCGACATGGCG 39
                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAX36283 from: 1 to: 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2b(7); 88pp; English.
                      Fig 12a; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harberd NP, Peng J, Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-485-529-104 x AAX36283
                                                                                                                                                                                                                                                                                               Quality: 62.00
Ratio: 4.769
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                    alignment_scores:
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit: growth of the plant. This growth inhibition is antagonised by globerellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are products can be to produce Rht mutant plants which are resistive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin blosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was contained after partially sequencing wheat Rht clone 14al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding Hevea brasiliensis (S)-hydroxy:nitrilase - useful for production of cyanohydrin(s) from aldehyde and hydrogen cyanide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (S)-hydroxynitrilase; production;(S)-cyanohydrin; aldehyde;hydrogen cyanide; recombinant;ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes Hevea brasiliensis (S)-hydroxynitrilase (S-HN), useful in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT86824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 309 BP; 47 A; 102 C; 102 G; 45 T; 13 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= (S)-hydroxynitrilase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hevea brasiliensis (S)-hydroxynitrilase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 GlyTyrLysValArgAlaSerAspMet 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 GGGTACAAGGTGCGCGCCTCCGACATG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAX36261 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (OSTS ) CHEMIE LINZ DEUT GMBH IL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAT86824 standard; cDNA; 817 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 8; 8pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95DE-1029116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-485-529-104 x AAX36261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio: 5.111
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-155423/15.
P-PSDB; AAW29164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hevea brasiliensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE19529116-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT86824;
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Recombinant S-HN has higher specific activity

and ketone.

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vea brasiliensis S-hydroxy:nitrilase - and recombinant equivalent
high specific activity, for chiral synthesis of cyano:hydrin(s)
(S)-cyanohydrins from aldehyde and hydrogen cyanide. Recombinantly produced S-HN has higher specific activity than native S-HN, probably due to post translational modification differences between plants and microoranisms.

S-HN was isolated from H. brasiliensis leaves by homogenisation, followed by sequential chromatography on QAE-Sepharose FF, Phenyl-Sepharose and Biogel P180. A cDNA bank from the same source was prepared and screened with polyclonal rabbit antiserum raised against the isolated enzyme. The insert, about 1.1 kb, in the single positive clone was cloned into pHNLL00 and sequenced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes the Hevea brasiliensis
S-hydroxynitrilase (S-HN), which can be used for the chiral
synthesis of aliphatic or aromatic S-cyanohydrins from HCN, or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schall M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-hydroxynitrilase; chiral synthesis; aliphatic; aromatic; S-cyanohydrin; recombinant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT36351
                                                                                                                                                                                 Sequence 817 BP; 250 A; 159 C; 193 G; 215 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       116 CTCCTTGAGGCACTTGGCCACAAGGTTACTGCACTGGACCTTGCA 160
                                                                                                                                                                                                                                                                                                                                                                                      3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                                                                                            Length: 15
Gaps: 0
Percent Identity: 66.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= S-hydroxynitrilase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hevea brasiliensis S-hydroxynitrilase cDNA.
                                                                                                                                                                                                                                                                                                                                                        to: 817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
57..830
                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAT86824 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Pages 2-3; 14pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID AAT36351 standard; cDNA; 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STAM ) DSM CHEMIE LINZ GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-EP03010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95AT-0001182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griengl H, Hasslacher M,
                                                                                                                                                                                                                                           45.00
3.750
80.000
                                                                                                                                                                                                                                                                                                                          US-09-485-529-104 x AAT86824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hevea brasiliensis.
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                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                              Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-1995;
                                                                                                                                                                                                                               alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schwab H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT36351;
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than the native enzyme.

H. brasiliensis leaves were homogenised in cold pH 6.5 K phosphate buffer, and the extract subjected to sequential chromatography on OAB-Sepharose. Phenyl-Sepharose and BioGel 150 to recover a protein with a specific activity of 19 IU/mg.

A CDNA library was prepared from young H. brasiliensis leaves in Zap phage, and screened with polyclonal rabbit antiserum raised against the purified enzyme. The insert in one positive clone was isolated, and ligated into pBluescript to form pHNL-100. This plasmid, in E. coli SOLK, expressed a fusion protein with lacz that was immunoreactive. Sequencing showed that the insert in this plasmid was not complete, and the missing 5'-end generated by 2 stage PCR, resulting in plasmid pHNL-101, containing the entire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= "Keratan sulphate 6-sulphotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSGal6ST; keratan sulphate 6-sulphotransferase; hybridization;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chick chondroitin 6-sulphotransferase; C6ST; phage Lambda; expression vector; COS-7 cells; Bluescript plasmid; galactose; keratan sulphate; chondroitin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keratan sulphate 6-sulpho-transferase polypeptide - transfers sulphate from sulphate donor to galactose 6-hydroxy group etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV36418
                                                                                                                                                                                                                                                               Sequence 1091 BP; 326 A; 196 C; 239 G; 330 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 CTCCTTGAGGCACTTGCCACAAGGTTACTGCACTGGACCTTGCA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                                                                                                                                                                              Length: 15
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keratan sulphate 6-sulphotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID AAV36418 standard; cDNA; 1458 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SEGK ) SEIKAGAKU KOGYO CO LTD.
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                                                                                                                                                                                                                                                                                                                                45.00 · 3.750 80.000
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US-09-485-529-104 x AAT36351
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAT36351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-288750/26.
P-PSDB; AAW61100.
                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                  coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-NOV-1996;
                                                                                                                                                                                                                                                                                                                  alignment_scores:
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Dreier H;

Pesch S,

Elbers K,

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This nucleic acid sequence is a cDNA coding for human KSGal6ST (Keratan sulphate 6-sulphotransferase). The sequence was obtained by radiolabelling the cDNA of chick chondroitin 6-sulphotransferase (C6ST) and using this as a probe in a random oligonuclectide primed labelling method. Human foetal brain cDNA was inserted into a phage Lambda gtll clone; where the clones containing the KSGal6ST were obtained by hybridization using the prepared probe. The positive clones were subcloned into a recombinant expression vector and used to transform cost. The positive from which calls expressing KSGal6ST was nbe selected. The phage cDNA inserts were isolated and subcloned into a Bluescript plasmid. Deletion clones were then prepared from which both strands were sequenced betton clones method. The KSGal6ST of the invention transfers the sulphate from a sulphate donor to galactose 6-0H groups in keratan compliante, but does not transfer sulphate to chondroitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porcine reproductive and respiratory syndrome; PRRS; pig; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "especially preferred attenuation site (codon for Tyr-946)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porcine reproductive and respiratory syndrome virus ORF1b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH26333
                                                                                                                                                                                                                                                                                                                                  Sequence 1458 BP; 254 A; 526 C; 421 G; 257 T; 0 other;
                                                                                                                                                                                                                                                                                                 sulphate A or C, dermatan sulphate or CDSNS heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           syndrome virus
                                                                                                                                                                                                                                                                                                                                                                                                       Length: 14
Gaps: 0
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
200ce- Preferred attenuation site"
2936..2838
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAV36418 from: 1 to: 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porcine reproductive and respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; infection; attenuation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
2806..2868
                  Claim 9; Page 15-16; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _documentation_block:
AAH26333 standard; DNA; 4374 BP.
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26-JAN-2000; 2000DE-1003372.
26-JAN-2000; 2000DE-1003373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-2001; 2001WO-EP00865.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-485-529-104 x AAV36418
                                                                                                                                                                                                                                                                                                                                                                                                     44.00
3.667
85.714
                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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The present sequence is that of open reading frame (ORF) 1b of porcine reproductive and reapiratory syndrome (PRRS) virus strain ATCC VR-2332. It encodes a 1457 annio acid viral protein (see AAB82665). The invention provides live attenuated PRRS viruses which are attenuated by at least 1 amino acid mutation in a specific site of the viral protein coded by ORF 1b or ORF 2. A claimed live attenuated PRRS virus has at 1 east 1 of the amino acids in positions 321-341 of the ORF1a-encoded protein (see AB82655), and/or at least 1 of the amino acids in positions 321-341 of the amino acids in positions 1-20 of the ORF 2-encoded protein (see AB82657) deleted. Of the ORF 1b-encoded protein, and/or at least 1 of the amino acids in positions 1-20 of the ORF 2-encoded protein (see AAB82667) deleted. Other claimed live attenuated PRRS viruses have amino acid 31 of ORF2 deleted or replaced by an amino acid ont identical to that of ARCC VR-2332. Specific mutations are created using molecular cloin are also claimed. The live attenuated PRRS viruses are used in the manufacture of a vaccine for the prophylaxis and treatment of PRRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porcine reproductive and respiratory syndrome virus; PRRSV; vaccine; plg; attenuated virus; \ensuremath{\mathrm{ds}} .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viruses that are less
                                                                                                                        οğ
                                                                                                  Novel live porcine reproductive and respiratory syndrome virus attenuated by mutations in specific site of viral protein coded specified open reading frames, useful for prophylaxis/treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1690 GACAGGATCCTCGCGGCCCTCGCCTATCACATGAAGGCGAGTAATGTTTC 1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4374 BP; 1026 A; 1197 C; 1109 G; 1042 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC81763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porcine Lelystad virus MSV JA-142 attenuated version.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections in pigs. Infectious clones of PRRS virus virulent than VR-2332 can be recombinantly produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 17
Gaps: 0
Percent Identity: 47.059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: AAH26333 from: 1 to: 4374
                                                                                                                                                                                                       Disclosure; Fig 5a-c; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID AAC81763 standard; DNA; 15424 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-485-529-104 x AAH26333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.00
2.750
94.118
                                    WPI; 2001-483237/52.
P-PSDB; AAB82666.
                                                                                                                                                              viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lelystad virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200065032-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-NOV-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 a 17
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15-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2000
                                                                                                                                                                                                                                                                                                   alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA27809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 a 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             North
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cos
The present invention provides a novel method of producing attenuated versions of viruses, using multiple passage through cell cultures and involving the removal of samples of the virus prior to the induction of cytopathic effects. The sample is then inoculated into the next cell culture. The sequence of the naturally-occurring Lelystad virus (also known as the porcine reproductive and respiratory syndrome virus or PRRSV) atypical strain JA-142 is provided, along with that of a modified version of the virus. The modified version can be used in the vaccination of pigs against the Lelystad virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reproductive and respiratory syndrome virus; PRRSV; vaccine; pig;
                                                                                  Gorcyca DE;
                                                                                                                          Passaging viruses to attenuation comprises maintaining virus in logarithmic phase of replication throughout multiple cell culture passages, useful for protection against atypical porcine reproductive and respiratory syndrome virus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15424 BP; 3380 A; 4083 C; 4008 G; 3953 T; 0 other;
                                                                                  Burkhart K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC81764
                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 47.059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porcine Lelystad virus JA-142 virulent version.
                                                                                  Roof M,
                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                to: 15424
                                                                                                                                                                              Example 7; Page 56-61; 70pp; English.
                                                                                  Lager K,
                                                                                                                                                                                                                                                                                                                                                                                                                               to: AAC81763 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID AAC81764 standard; DNA; 15424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000WO-US10852.
        21-APR-2000; 2000WO-US10852.
                            99US-0298110.
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                                                                                 Vorwald A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                     44.00
2.750
94.118
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US-09-485-529-104 x AAC81763
                                                            (USDA ) US SEC OF AGRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attenuated virus; ds
                                                                                                     WPI; 2000-687328/67
                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200065032-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lelystad virus
                                                                                 Mengeling WL,
                              22-APR-1999;
                                      15-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-1999;
                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 a 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porcine
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The present invention provides a novel method of producing attenuated versions of viruses, using multiple passage through cell cultures and involving the removal of samples of the virus prior to the induction of cytopathic effects. The sample is then inoculated into the next cell culture. The sequence of the naturally-occurring Lelystad virus (also known as the porcine reproductive and respiratory syndrome virus or PRRSV) atypical strain JA-142 is provided, along with that of a modified version of the virus. The modified version can be used in the vaccination
                                                                                                         Gorcyca DE;
                                                                                                                                                                                                                 Passaging viruses to attenuation comprises maintaining virus in logarithmic phase of replication throughout multiple cell culture passages, useful for protection against atypical porcine reproductive and respiratory syndrome virus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   syndrome virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  North American porcine reproductive and respiratory syndrome virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   North American PRRS virus; Nidovirales virus; pig; swine; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag- b
/note- "ORPD, encodes polyprotein comprising
replicase (RNA polymerase) and helicase
functions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "ORFla, encodes polyprotein comprising
protease function"
7664..12055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15424 BP; 3370 A; 4075 C; 4011 G; 3968 T; 0 other;
                                                                                                         Roof M, Burkhart K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA27809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 17
Gaps: 0
Percent Identity: 47.059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 15424
                                                                                                                                                                                                                                                                                                                                                    Example 7; Page 61-66; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      American porcine reproductive
                                                                                                         Lager K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
192..7685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of pigs against the Lelystad virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA27809 standard; cDNA; 15450
99US-0461879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                         Vorwald A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.00
2.750
94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-485-529-104 x AAC81764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAC81764
                                                      OF AGRIC
                                                                                                                                                             WPI; 2000-687328/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
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                                                      (USDA ) US SEC
                                                                                                         Mengeling WL,
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encodes small membrane glycoprotein"

encodes small membrane glycoprotein

/note- "ORF3, 13225..13761

/*tag=

note= "ORF2,

/*tag=

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CDS
   CDS
    CDS
CDS
 cos
CDS
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The present sequence is that of cDNA corresponding to the North American porcine reproductive and respiratory syndrome (PRRS) virus isolate P129A RNA genome. The cDNA in plasmid p77129A is deposited as ATCC 20348B. The P129 virus was originally isolated from a struck p129A was obtained after 10 serial passages from the pig. The DNA sequence includes B oper reading frames (ORFS 1a, 1b, 2-7) encoding polyproteins comprising protease, replicase and helicase functions, small membrane proteins a major envelope corporation, an integral membrane protein and a nucleocapsid protein. The invention provides isolated polynucleotide molecules, plasmids, viral vectors and transfected host cells that comprise plasmids, viral vectors and transfected host cells that comprise molecules, viral vectors and transfected host cells encoding genetically modified North American PRRS viruses that are disabled in their ability to cause PRRS. The invention also provides comprises comprising such plasmids, Narolecules, viral vectors and contens and morth American PRRS viruses that are disabled in their ability to cause PRRS. The invention also provides cand North American PRRS viruses that are disabled and North American PRRS viruses, viral vectors and enthods of using these a genetically modified North American PRRS viruses may also comprise a genetically modified North American PRRS viruses of using these a genetically modified North American PRRS viruses of using these a genetically modified North American PRRS viruses of using these a genetically modified North American PRRS viruses of using these a genetically modified North American PRRS viruses of using these a genetically modified North American PRRS viruses of using these a genetically modified North American PRRS viruses of using these and pertention of the viruses of the province of the virus of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide encoding an infectious RNA molecule of a North
American porcine reproductive and respiratory syndrome virus for use as
a vaccine in protecting swine and other animals from infection by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      more heterologous antigenic epitopes, or a plasmid encoding such a PRRS virus. Also provided are isolated polynucleotide molecules, viral vectors, and transfected host cells that comprise a nucleotide sequence encoding a peptide of a North American PRRS virus. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are useful in providing peptides to compensate for mutated peptide coding sequences of DNA sequences encoding genetically modified North American PRRS viruses so that functional virions can be
/noté= "ORF4, encodes small membrane glycoprotein"
13772..14374
                                                                                                                                                                                                              "ORF5, encodes major envelope glycoprotein"
                                                                                                                                                                                                                                                                                                                                                                         /note= "ORF6, encodes nonglycosylated integral
membrane protein"
14873..15244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= h
/note= "ORF7, encodes nucleocapsid protein"
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                                                                                                                                                                                                                                                                             .4359..14883
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                                                                                                                                                                                                                               'note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-2000
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Sequence 15450 BP; 3398 A; 4060 C; 4041 G; 3951 T; 0 other;

The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by the treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which has products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. Primers AAX36234-X36254 were used in the sequencing of maize D8 gene (a homologue of the Rht gene) clones, in the course of the invention.

Claim 50; Page 52; 88pp; English.

Sequence 29 BP; 5 A; 5 C; 11 G; 8 T; 0 other;

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New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                              Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; D8 gene; maize; sequencing primer; ss.
                                                                                                                   1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36248
                                                                                                                                                                                                                                                                                           Primer used for sequencing of the maize D8 gene clones.
      Length: 17
Gaps: 0
Percent Identity: 47.059
                                                                                  to: 15450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE;
                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peng J, Richards
                                                                                                                                                                                                               seq_documentation_block:
ID AAX36248 standard; DNA; 29 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PLAN-) PLANT BIOSCIENCE LTD.
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                                                                                                                                                                                                                                                                     16-JUL-1999 (first entry)
       44.00
2.750
94.118
                                                  alignment_block:
US-09-485-529-104 x AAA27809
                                                                                  Align seg 1/1 to: AAA27809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-181040/15.
          Quality:
Ratio:
                             Percent Similarity:
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                       9421 T 9421
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990s - 013722

990s - 013722

990s - 0137528

990s - 0137724

990s - 0137724

990s - 0137724

990s - 0139452

990s - 0139452

990s - 0139455

990s - 0139455

990s - 0139455

990s - 0139456

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990s - 0139456

990s - 0139463

990s - 0142970

990s - 0142970

990s - 0144085

990s - 0144085

990s - 0144331

990s - 0144332

990s - 0144332

990s - 0144334

990s - 0144336

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990s - 014508

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03-AUG-1999;
04-AUG-1999;
28 - MAY - 1999,
01 - JUN - 1999,
03 - JUN - 1999,
04 - JUN - 1999,
08 - JUN - 1999,
10 - JUN - 1999,
14 - JUN - 1999,
16 - JUN - 1999,
16 - JUN - 1999,
18 - JUN - 1999,
18 - JUN - 1999,
                                                                                                                                                                                     18 - JUN - 1999;
18 - JUN - 1999;
18 - JUN - 1999;
18 - JUN - 1999;
18 - JUN - 1999;
18 - JUN - 1999;
18 - JUN - 1999;
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P-PSDB; AAW24618
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The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ONF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ONF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide
                                                                                                                                                                                                                                                                                                               Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
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                                    Percent Identity: 60.000
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                         Gaps:
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                                                                                                   from: 1
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This sequence encodes a H. pylori inner membrane protein.
Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are also useful for generating vaccines for immunising subjects against H.
production, e.g. in E. coli hosts.
Note: This DNA sequence is not reproduced in the specification and has
been derived from the related specification, WO9719098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisense; inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori nucleic acid sequences and related proteins used for diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_except= (pos: 868..870, aa: Xaa)
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22-JUL-1999;
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9-JUL-1999
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                                                                                                                                                                                                                                                                                                                                             -NDC-81
      pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique batxII-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts shotgun subclone libraries. The purified DNA samples were then
                                                                                                                  Note: The ORF/protein reference number for this sequence was obtained from the related specification, WO9640893.
                                                                                                                                                                                                                                                                                                                                                                                                                      Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC47916
                                                                                                                                                                                                                                                                                     2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                 Sequence 894 BP; 316 A; 150 C; 170 G; 256 T; 2 other
                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AAT77436 from: 1 to: 894
                                                                                                                                                                                     Length: 16
Gaps: 0
Percent Identity: 37,500
                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana DNA fragment SEQ ID NO: 55584.
                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-485-529-104 x AAT77436/rev
                                                                                                                                                                                   42.00
2.800
93.750
                                                                                                                                                                                              Ratio:
Percent Similarity:
                                                                                                                                                                                       Quality:
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Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFs are shown. The proteins are variously cell envelope proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori nucleic acids and proteins - used to develop products for the detection, prevention and treatment of H. pylori infections
                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAX30475
                                                                                                                                                                                                                                                                                                                                                                                  H. pylori secreted protein ORF hp6p10606_23493756_c1_21.
                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine; probe; diagnostic; ORF; cell envelope protein; secreted protein; cellular protein; ds.
                                                                                                                                                                                                                                                                       Percent Identity: 60.000
                                                                                                                                                                        Length:
                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                         Align seg 1/1 to: AAC47916 from: 1 to: 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claims 3, 4; Page 137; 279pp; English.
                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID AAX30475 standard; DNA; 1464 BP.
        990S - 0160815
990S - 0160815
990S - 0160980
990S - 0160989
990S - 0161404
990S - 0161406
990S - 0161359
990S - 0161360
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96US-0739150.
96US-0759739.
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 99US-0160770
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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3.500
80.000
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P-PSDB; AAY11008.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alm RA, Smith D;
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                                                                                                                                                                         Quality:
Ratio:
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28-OCT-1996;
06-DEC-1996;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
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25-0CT-1999;
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28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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                                                                                                                                                                 alignment_scores
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  990S - 0145089
990S - 0145185
990S - 0145185
990S - 0145186
990S - 0145214
990S - 0145218
990S - 0145918
990S - 0145919
990S - 0145919
990S - 014703
990S - 014704
990S - 0147304
990S - 0147305
990S - 0148311
990S - 0149308
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990S-0157865.
990S-0158029.
990S-0158232.
990S-0158289.
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9905-0150884-
9905-0151065-
9905-0151065-
9905-0151080-
9905-0151438-
9905-0151438-
9905-015305-
9905-015307-
9905-0154018-
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9905-0154018-
9905-0154608-
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9905-0154608-
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99US-0159329.
99US-0159330.
99US-0159331.
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99US-0160767.
99US-0160768.
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99US-0156596.
99US-0157117.
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99US-0159638.
99US-0159584.
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28 - JUL - 1999
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09-AUG-1999;
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27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
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08-0CT-1999;
12-0CT-1999;
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13-0CT-1999;
14-0CT-1999;
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14-0CT-1999;
14-0CT-1999;
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22-JUL-1999;
23-JUL-1999;
23-JUL-1999;
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21-OCT-1999;
21-OCT-1999;
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16-AUG-1999;
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18-AUG-1999;
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23-AUG-1999
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secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         es and related
treat or prevent H. pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes a H. pylori inner membrane protein. The protein may be used in a vaccine to prevent or treat H. pylori
                                                                                                                                                                                                                                                                                                                                                                     611 GAGATTTTAACATCATTAGGATTTAGGATAAGAATGTCTAATTTGTCT 564
                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT68140
                                                                                                                                                                                                                                                                                                                                                 2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                             Sequence 1464 BP; 545 A; 273 C; 276 G; 370 T; 0 other;
                                                                                                                                                                                                                                                                                                                       to: 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. pylori inner membrane protein ORF 13ep12003orf20.
                                                                                                                                                                                                          Length: 16
Gaps: 0
Percent Identity: 37.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1..1554
/*tag= a
/note= "no stop codon given"
                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori nucleic acid sequences polypeptide(s) - useful for vaccines to trinfection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                  to reverse of: AAX30475
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                                                                                                                                                                                                                                                                                      US-09-485-529-104 x AAX30475/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT68140 standard; DNA; 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0630405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-1997 (first entry)
                                                                                                                                                                                                                       2.800
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                                                                                                                                                                                                          42.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-052306/05.
P-PSDB; AAW20887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB.
                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis; ds
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                                                                                                                                                                                           alignment_scores
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                                                                                                                                                                                                                                                                                                                  Align seg 1/1
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infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55/59) was determined from coverlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; Helicobacter infection; gastroduodenal disease; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             develop products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Helicobacter polynucleotides - used to develop
for the diagnosis, prevention and treatment of Helicobacter
infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomb J;
                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAX14024
                                                                                                                                                                                                                                                                                                                                                                                                                    2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                                                           Sequence 1554 BP; 571 A; 281 C; 290 G; 412 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                       to: 1554
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Gaps: 0
Percent Identity: 37.500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
51..1514
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: AAT68140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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ID AAX14024 standard; DNA; 1564
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97US-0833457.
97US-0881227.
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US-09-485-529-104 x AAT68140/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptic ulcer disease; ss.
                                                                                                                                                                                                                                                                       42.00
2.800
93.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. pylori GHPO 479 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         delicobacter pylori.
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                                                                                                                                                                                                                                                                         Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1998;
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                                                                                                                                                                                                                                                          alignment_scores:
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24-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX14024;
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Claim 1; Page 391-394; 2054pp; English.

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This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcr diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and its flanking regions was determined (AAQ66797). The spheroidin gene can be used as the location for insertion of heterologous DNA in insect and mammalian expression systems. A spheroidin-like gene was also identified in CDEPV and its amino acid sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New entomopoxvirus polynucleotide sequences, proteins and vectors - are used for expression of heterologous proteins in both insect and mammalian host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence of the Amsacta moorel entomopoxvirus spheroidin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spheroidin; gene expression; vector; insect cell culture;
                                                                                                                                                                                                                                                                                                                                                                                                                   661 GAGATTTTAACATCACTAGGGTTTAGGATAAGAATGTCTAATTTGTCT 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ66825
                                                                                                                                                                                                                                                                                                                                                                                  2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                Sequence 1564 BP; 576 A; 285 C; 294 G; 409 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: AAX14024 from: 1 to: 1564
                                                                                                                                                                                                                              Laugen: 16
Gaps: 0
Percent Identity: 37,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     culture; AmEPV; CbEPV; Amsacta moorei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Choristoneura biennis entomopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 87; 118pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moyer RW
                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-485-529-104 x AAX14024/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ66825 standard; DNA; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0991867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-US11907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-1995 (first entry)
                                                                                                                                                                                                                              42.00
2.800
93.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CbEPV spheroidin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hall RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-217887/26
                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                  alignment_scores
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and its flanking regions was determined (AAQ66797). The spheroidin gene can be used as the location for insertion of heterologous DNA in insect and mammalian expression systems. A spheroidin-like gene was also identified in CfEPV and its amino acid sequence was deduced (AAR55587).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New entomopoxvirus polynucleotide sequences, proteins and vectors - are used for expression of heterologous proteins in both insect and mammalian host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of the Amsacta moorei entomopoxvirus spheroidin gene
                                                                                                                                                                                                                                                                                                                                   Spheroidin; gene expression; vector; insect cell culture; mammal cell culture; AmEPV; CfEPV; Amsacta moorei;
                                                                                                                                                                                   seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ66826
         Length: 14
Gaps: 0
Percent Identity: 64.286
                                                                                                                                            Percent Identity: 64.286
                                                                                                                              73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                         Choristoneura fumiferana entomopoxvirus
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2
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ö
                                                                                                     Align seg 1/1 to: AAQ66825 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAQ66826 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 235 BP; 95 A; 25 C; 42
                                                                                                                                                                                                                             ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93WO-US11907.
                                                                                                                                                                                                               seq_documentation_block:
ID AAQ66826 standard; DNA; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-0991867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moyer
                                                                                                                                                                                                                                                                                (first entry)
                                                                alignment_block:
US-09-485-529-104 x AAQ66825
           41.00
3.727
78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.00
3.727
78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-485-529-104 x AAQ66826
                                                                                                                                                                                                                                                                                                         CfEPV spheroidin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gruidl ME, Hall RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-217887/26.
                                                                                                                                                                                                                                                                                                                                                             entomopoxvirus; ss
            Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1993;
                                                                                                                                                                                                                                                                                18-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                  WO9413812-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUN-1994
                                                                                                                                                                                                                                                      AAQ66826
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2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15

Seguence 235 BP; 96 A; 20 C; 42 G; 77 T; 0 other;

US-09-485-529-104 x AAZ10092

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The present squares to make the expression systems of the invention. The specification describes an EPV expression system that is capable of directing the replication and expression of a heterologous gene in a selected host cell. The expression system comprises an EPV promoter sequence operably linked to the selected heterologous gene in a selected host cell. The expression of a heterologous sequence operably linked to the selected heterologous gene sequence operably linked to the spected heterologous gene heterologous sequences and the production of selected proteins in insect and mammalian host cells e.g. human, rodent and primate cells. EPV thymidine kinase and spheroidin genes can also be used in vertebrate poxitruses such as vaccinia and swinepox virus. The expression vectors can also be used for the control of insect pests through the insertion of a gene encoding an insect toxin into the capression vector which will infect the target pest and produce large quantities of the toxin. Spheroidin and thymidine kinase are nonessential proteins which makes them ideal for the insertion of exogenous DNA and they are capable of operating in a vertebrate poxvirus (e.g. vaccinia)-mammalian cell-mediated and humoral immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents an Entomopoxvirus (EPV) spheroidin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vel expression system for the expression of heterologous sequences insect and mammalian host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spheroidin; Entomopoxvirus; expression system; replication; heterologous gene expression; thymidine kinase; poxvirus; vaccinia; swinepox virus; insect pest control; immunity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Choristoneura biennis entomopoxvirus spheroidin-like gene sequence.
                                                                                                             seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ10092
Example 10; Column 99-102; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moyer RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choristoneura biennis entomopoxvirus.
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                                                                                                                                                                                     documentation_block:
AA210092 standard; DNA; 235 BP.
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91US-0657584.
92US-0827685.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0544332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-US00855
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                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hall RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-457596/38.
P-PSDB; AAY30179.
                                                                                                                                                                                                                                                                                                                                                                   28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-1991;
30-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5935777-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-0CT-1995
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                                                                                                                                                                                                                                                                                               AAZ10092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel
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Sequence 235 BP; 96 A; 20 C; 42 G; 77 T; 0 other;
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The present sequence represents an Entomopoxvirus (EPV) spheroidin-like gene sequence. It is used to make the expression systems of the invention. The specification describes an EPV expression system that is capable of directing the replication and expression of a heterologous gene in a selected host cell. The expression system comprises an EPV promoter sequence operably linked to the selected heterologous gene promoter sequence operably linked to the selected heterologous gene capaned. The expression system is used for the expression of heterologous sequences and the production of selected proteins in insect and mammalian host cells e.g. human, rodent and primate cells. EPV thymidine kinase and spheroidin genes can also be used in vertebrate poxviruses such as vaccinia and swinepox virus. The expression vectors can also be used for the control of insect pest the insertion of a gene encoding an insect toxin into the expression vector which will infect the target pest and produce large proteins which makes them ideal for the insertion of exogenous DNA and they are capable of operating in a vertebrate poxvirus (e.g. vaccinia) and thymidine kinase are able to mammalian cell expression vector system. Pox viruses are able to
                                                                                                                                                                                                                                                                       Choristoneura fumiferana entomopoxvirus spheroidin-like gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel expression system for the expression of heterologous sequences in insect and mammalian host cells
                                                                                                                                                                                                                                                                                                                        heterologous gene expression; thymidine kinase; poxvirus; vaccinia; swinepox virus; insect pest control; immunity; ss
                                                                                                                                                                                                                                                                                                           Spheroidin; Entomopoxvirus; expression system; replication;
                                                                                                        seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ10093
                                                      2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Column 101-102; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   Choristoneura fumiferana entomopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moyer RW;
 ;
to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stimulate cell-mediated and humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYFL ) UNIV FLORIDA RES FOUND INC.
from: 1
                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0544332.
91US-0657584.
92US-0827685.
92WO-US00855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li Y,
                                                                                                                                            seq_documentation_block:
ID AA210093 standard; DNA; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0544332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0991867
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hall RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-457596/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAY30180
 ;
to
                                                                                                                                                                                                                                     28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-0CT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                        US5935777-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .9-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-1992
12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gruidl ME,
Align seg 1/1
                                                                                                                                                                                                 AAZ10093;
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Sequence 235 BP; 95 A; 25 C; 42 G; 73 T; 0 other;

Length: 14 Gaps: 0 Percent Identity: 64.286

41.00 3.727 78.571

Ratio:

Quality:

alignment_scores

Percent Similarity:

alignment_block:

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence was dwarf but let crop plants grow tall. The present sequence was cobtained after partially sequencing wheat Rht clone 5al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence obtained after sequencing wheat Rht clone 5al.
                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 285 BP; 39 A; 89 C; 100 G; 46 T; 11 other;
                                      Percent Identity: 64.286
                                                                                                                                                                                                                 84 GAATTATTGAACGTCAAAGGTTATCCTGTTAAAGCATCCGAT 125
                                                                                                                                                                          2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
Length:
                                                                                                                                  Align seg 1/1 to: AAZ10093 from: 1 to: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2c(4); 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harberd NP, Peng J, Richards DE;
                                                                                                                                                                                                                                                                                                             AAX36271 standard; DNA; 285 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97GB-0017192.
                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-1999 (first entry)
                  3.727
                                                                                              US-09-485-529-104 x AAZ10093
  41.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-181040/15.
                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          paclobutrazol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum
  Quality:
                    Ratio:
                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PLAN-) PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9909174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999
                                                                              aliqnment block:
                                                                                                                                                                                                                                                                                                                                                   AAX36271;
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Gaps: 0 Percent Identity: 88.889

41.00 5.125 88.889

Quality: Ratio:

alignment_scores:

Percent Similarity:

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AAM25966 to AAM99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and calls they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system, virucide; antibacterial; endocrine; cardiant; cardiovascular; antianaemic; antiaggregant; hammostatic; vulnerary; antiuloer; osteopathic; dermatological; antialergic; antiasthmatic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective, antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine, inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; asthma; allergic rhinitis; diabetes; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; heurological disorder; so, neurodegenerative disorder; neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antiboterial; endocrine; cardiant; central nervous system; Virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                              seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH99418
                                                           to: 285
                                                                                                                                                                                                                                                                                                                                                                                                Human protein encoding cDNA sequence SEQ ID NO:253.
                                                           from: 1
                                                           to reverse of: AAX36271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 410; 1217pp; English.
                                                                                                                                                   283 GGGTACAAGGNGCGCGCATCNGACATG 257
                                                                                                       8 GlyTyrLysValArgAlaSerAspMet 16
                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                          seq_documentation_block:
ID AAH99418 standard; cDNA; 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rang YT, Liu C, Drmanac RT;
                  US-09-485-529-104 x AAX36271/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-2000; 2000WO-US35017
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-457603/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAM25477
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                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001
alignment_block:
                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                           AAH99418;
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The present invention describes a purified or isolated nucleic acid sequences (I) consisting essentially of one of the 93 nucleotide sequences given in AAH81202 to AAH81294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism. (I) have antibacterial and antibiotic activities, and can be used in gene therapy. Expression of (I) in a microorganism inhibits proliferation of the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used
rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic diseaders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhintitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli protein encoding nucleotide sequence SEQ ID NO:262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids encoding proteins required for Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli; identification; proliferation; microorganism; antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis; bacterial growth inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferation, useful for screening for antimicrobial agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH81463
                                                                                                                                                                              Sequence 556 BP; 153 A; 125 C; 128 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                    556
                                                                                                                                                                                                                                                                                                   Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 ATGATGCCACCATTGGGATACAGTGTGAAAAGCAGCACATTG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16
                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                            Length:
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                                                                                                                                                                                                                                                                                                                                                                                                    to reverse of: AAH99418
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US-09-485-529-104 x AAH99418/rev
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3.154
92.857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
AAH81463 standard; 1
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                                                                                                                                                                                                                                                            Quality:
Ratio:
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                                                                                                                                                                                                                                                                                               Percent Similarity:
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as antisense therapeutics for killing bacteria. In addition to rherapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. AAH81035 to AAH81487 encode the Escherichia coli proteins given in AAG98239 to AAH81487 and AAH81488 to AAH81491 represent oligonucleotides, which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine;
antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
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Scalato E, Scarselli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria gonorrheae ORF 092 partial DNA sequence SEQ ID NO:309
                                                                                                                                                                                                                                                                                                                                                                               109 GAAGITCIGGCCAAIGAAGGITATCAGATCAGIGGITCCGAITIAGCG 156
                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ53179
                                                                                                                                                             other;
                                                                                                                                                                                                                                                                                                                                                     2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla
                                                                                                                                                                                                                  Length: 16
Gaps: 0
Percent Identity: 50.000
                                                                                                                                                            Sequence 1476 BP; 330 A; 372 C; 436 G; 338 T; 0
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Ratti
                                                                                                                                                                                                                                                                                                                        to: 1476
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Rappuoli R,
                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAH81463 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibacterial; gene therapy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ53179 standard; DNA; 1521
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98US-0103796.
99US-0121528.
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US-09-485-529-104 x AAH81463
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                                                                                                                                                                                                                                 3.154
81.250
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                                                                                                                                                                                                                     41.00
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P-PSDB; AAY74417.
                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
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                                                                                                                                  present invention.
                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                    Ratio
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09-OCT-1998;
25-FEB-1999;
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Tettelin H,
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AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54571 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also be used in gene therapy protocols.
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antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
antibacterial; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masignani V, Mora M;
Scalato E, Scarselli M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ53180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1521 BP; 359 A; 430 C; 394 G; 338 T; 0 other;
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Gaps: 0
Percent Identity: 56.250
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Ratti G,
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Claim 7; Page 288; 1453pp; English.
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, Pizza M, Rappuoli R,
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AAZ53180 standard; DNA; 1521 BP.
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98US-009894.
98US-0103749.
98US-0103794.
98US-0103796.
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3.154
81.250
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US-09-485-529-104 x AAZ53179
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Venter JC;
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Ratio:
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Petersen J,
Tettelin H,
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09-0CT-1998)
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represent novel Neisseria menigitis and N. genorrheae polynucleotides and polypeptides. AAZ5457 to AAZ5576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as manufacture of medicaments for treating or preventing in the neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
                                                                                                           AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis ORF 092 partial DNA sequence SEQ ID NO:313.
                            Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AA253181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                                                                                                                                                                                     Sequence 1521 BP; 352 A; 444 C; 396 G; 329 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 56.250
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                                                                           Claim 7; Page 289; 1453pp; English
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98US-0094869.
98US-0098994.
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98US-0103749.
98US-0103794.
98US-0103796.
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(GENO-) INST GENOMIC RES.
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P-PSDB; AAY74418
                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
   Quality:
   Ratio:
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02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
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AAQ71977 is the DNA sequence of murine IL-2R gamma AAR59094, this was used in the development of a claimed method for the diagnosis of X-linked severe combined immunodeficiency (XSCID), in female carriers and male sufferers.
                                                                                                                                Diagnosis of x-linked severe combined immunodeficiency (XSCID) comprises detecting mutated IL-2R gamma gene, also vectors and transgenic animals containing the mutated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAS06754
                                                                                                                                                                                                                                                                             Sequence 1608 BP; 413 A; 434 C; 349 G; 412 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSer 14
                                                                                                                                                                                                                                                                                                                                                                                                                        to reverse of: AAQ71977 from: 1
                                                                                                                                                                                                                                                                                                                                 Length:
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                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                  Noguchi M;
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                                                                                                                                                                                  Example 1; Fig 7; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID AAS06754 standard; cDNA; 2730
                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-485-529-104 x AAQ71977/rev
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  93US-0031143.
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Clary D;
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P-PSDB; AAU03554.
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                                                                                                         P-PSDB; AAR59094
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  12-MAR-1993;
14-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54577 to AAZ54576 and AAZ54575 and AAZ54573 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisseria bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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  Masignani V, Mora M;
Scalato E, Scarselli
                                                                                          Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine IL2-R gamma; X-linked severe combined immunodeficiency; XSCID; interleukin; ss.
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25..82
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Percent Identity: 56.250
  Hickey E,
Ratti G,
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                                                                                                                               Claim 7; Page 290-291; 1453pp; English
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25..1134
 Fraser C, Galeotti C, Grandi G,
Petersen J, Pizza M, Rappuoli R,
Tettelin H, Venter JC;
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/note= "Putative"
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US-09-485-529-104 x AAZ53181
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                                                   2000-062150/05
                                                                 P-PSDB; AAY74419
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Ratio:
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Fraser C,
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to: 1608

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Nucleic acids encoding human kinase polypeptides, useful for preventing
                                                                               Human; protein kinase; PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martinez R;
Polynucleotide sequence encoding human protein kinase #54.
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diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections -

Example 1; Figure 1; 433pp; English.

AASO6701-AASO6757 encode for novel human protein kinases #1-57. The
novel protein kinases have been identified as members of the tyrosine
or serine/threonine kinase (PTK and STK) families. The polynucleotides
encoding protein kinases and the polypeptides may be used in the
prevention, diagnosis and treatment of diseases associated with
the prevention, diagnosis and treatment of disease associated with
the properlate kinase expression. For example, they may be used to treat
cancers (especially cancers of haematopolatic origin), cardiovascular
disease (e.g. atherosclercsis), metabolic disorders (e.g. diabetes),
immune related diseases (e.g. rheumatoid arthritis), neurological
disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. asthma), infectious
disorders (e.g. HIV) and reproductive disorders (e.g. infertility).
Additionally, polynucleotides encoding protein kinases may be
used for gene therapy and as DNA probes in diagnostic assays.
The protein kinase polypeptides may be used as antigens in the production
of antibodies against the protein kinases and in assays to identify
modulators of protein kinase expression and activity.

Sequence 2730 BP; 821 A; 516 C; 602 G; 791 T; 0 other;

alignment_scores:

41.00 Length: 14 3.154 Gaps: 0 92.857 Percent Identity: 50.000

alignment_block: US-09-485-529-104 x AAS06754/rev

Align seg 1/1 to reverse of: AAS06754 from: 1 to: 2730

3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16

us-09-485-529-104.p2n.rst

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EST402683 KV1 Medic
EST3998063 KV0 Medic
NFO18F10RRIF1000 No
NFO59C03ST1F1020 De
NFO13C08ST1F1000 De
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NF040G10STIF1000 De
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8 UI-R-BJ1-atw-b-10-0
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gb_est2:BF866629
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gb_est2:BI301187
gb_est1:BE660115
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gb_gss:CNS03KRV
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gb_est2:BG586532
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                                                                                                                                                 About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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1 (bases 1 to 644)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu.Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Mood, T.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Seq primer: AATTAACCTCACTAAAGGG
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Location/Qualifiers
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AUTHORS
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                   AF083303 AF083303 Drosophila me
AI494302 qy98e10 x1 NCI CGAP Br
BH085545 RPCI-24-310A2.TV RPCI-
AQ67492 HS_2161_A1_H01_T7C CIT
AW586740 EST318363 MHAM Medicaq
BF497115 AT11189.5prime AT Dros
AZ344778 IM0079E02F MOUSE 10kb
AQ037915 CIT-HSP-2325G5 TV CIT-
AA394318 25915 Lambda-PRLZ Arak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Geed coats"
/tissue_type="Geed coats"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBK-CMY, Site_1: EcoRI; Site_2: XhoI; This cona library was constructed from polyA+ enriched mRNA from green seed coats in mid to late developemental stage, average fresh weight 250 mg per seed. Traces of pod and embryo tissue also present. Complementary DNA was synthesized from mRNA using an XhoI-poly(dT)
linker-primer. EcoRI adopters were ligated to the blunt-ended coDNA fragments and the products were digested with XhoI for directional cloning into lambda ZAP Express vector. This lambda library was amplified once using E. coli host strain XLI Blue MRF'. Inserts were then subcloned by mass excision using ExAssist helper phage for conversion into phagemid vector pBK-CMY in E. coli host strain XLOLR."
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                              06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harvis,N., Chapman,B.P. and Gijzen,M.
Gene expression in developing soybean seed coats
Unpublished (2000)
Contact: Gijzen M
Agriculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada NSV 4T3
Fai: 519 457 1470
Fax: 519 457 3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 17
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                               BE659955 711 bp mRNA EST 1077 GmaxSC Glycine max cDNA, mRNA sequence. BE659955
    134 t
                                                                                                                                                3.5e+03
3.5e+03
3.5e+03
                                                              .5e+03
                                                                                                         5e+03
                                                                                                                          .5e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: gijzenm@dem.agr.ca.
Location/Qualifiers
1. Arganism="Glycine max"
Arganism="Alycine max"
Alycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 711
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1114.03
1114.03
1114.03
1113.98
1113.98
1113.98
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  37.00
37.00
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US-09-485-529-104 x BE659955
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Ratio: 4.765
Percent Similarity: 100.000
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                                                                                                                                                                                                                                 seq_name: gb_est1:BE659955
                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS BE659955
                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max
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                   gb_est1:AF083303
gb_est1:AI494302
gb_gss:BH085545
gb_gss:AQ774982
gb_est1:AK586740
gb_est2:BF497115
gb_gss:AZ344778
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                                                                                                                                                                   gb_gss:AQ037915
gb_est1:AA394318
                                                                                                                                                                                                                                                                                                               DEFINITION
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ORIGIN
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TITLE
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/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To see http://www.genome.clemson.edu/orders" 290 c 276 g 128 t
/clone="HV_CEMO19J17f"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HvCDNA0004 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 17
Gaps: 0
Percent Identity: 100.000
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1 AspGluLeuLeuAlaAlaLeuGlyTyrLySValArgAlaSerAspMetAl 17

09:57:56 2001

Thu Dec 20

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legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 4.588
Percent Similarity: 100.000
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US-09-485-529-104 x AV410222
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KEYWORDS
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                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryzae.

1 (Joases 1 to 263)
Sasaki,T., Miyao,A. and Yamamoto,K.
Rice CDNA from callus 1995
Onpublished (1995)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lotus japonicus
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 355)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a
                                                                                                                                                                                                                                                                                                                                                                                                                                305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasak1@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2000
                                                                                                  11-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AV410222 355 bp mRNA EST 23-MAY-2(
DEFINITION AV410222 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNa clone MWL069f02_r 5', mRNA sequence.
                                                                                                D39460 263 bp mRNA EST 11-N
RICSO803A Rice shoot Oryza sativa cDNA, mRNA sequence.
D39460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone_lib="Rice shoot"
/note="Etiolated shoot (8 days old)"
/ 64 c 116 g 35 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 78.00 Length: 17
Ratio: 4.588 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                         D39460.1 GI:568611
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US-09-485-529-104 x D39460
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                                                                                                                                                                                                Oryza sativa.
                                    seq_name: gb_est2:D39460
                                                                             seq_documentation_block:
                                                                                                                                                                                                                      Oryza sativa
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VERSION
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SOURCE
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                                                                                                                DEFINITION
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TITLE
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KEYWORDS
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Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores J.H.R., Inman, J.T., Weller, J.W. and May (G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library in published (2000) on Jul 14, 2000 this sequence version replaced gi:9195668. Contact: Korth K Dept. of Plant Pathology University of Arkansas 217 Plant Science Building, Fayetteville, AR 72701, USA Tel: 501 575 5191
                                                                    The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Kosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                       seq_documentation_block:
LOCUS BE321891 372 bp mRNA EST 21-DEC-2000
DEFINITION NF045B07IN1F1058 Insect herbivory Medicago truncatula cDNA clone
NF045B07IN 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GATGAGCTTCTGGCGGCTTTAGGTTACAAGGTGCGTTCCTCTGACATGGC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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Gaps: 0
Percent Identity: 94.118
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Medicago Genome Initiative accession:
Insert Length: 798 Std Error: 0.00
Plate: 045 row: B column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 355
DNA Res. 7 (2), 127-130 (20
20277479
Contact: Yasukazu Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
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78.00
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LOCUS AL369357
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 Quality:
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                                                                          alignment_block:
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ORGANISM
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KEYWORDS
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             /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF045B071N"
/clone="NF045B071N"
/clone="type="local and systemic leaves"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vergente"
/note="type="total aleaves of plants fed upon by spended M. truncatula leaves of plants fed upon by spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

53 a 66 c 72 g 81 t
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E (base) 1 to 388)

S Yammoto, K. and Sasaki, T.

Rice cDNA from callus 1997

Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8862, Japan
Tel: 81-298-38-7441
Fax: 11-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C27475 388 bp mRNA EST 06-AUG-1997 C27475 Rice callus cDNA Oryza sativa cDNA clone C51976_1A, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 others
                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 94.118
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="C51976_1A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="callus"
102 c 134 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C27475.1 GI:2311320
                                                                                                                                                                                                                                                                                                                                         Ratio: 4.588
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-485-529-104 x BE321891
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: BE321891
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LOCUS C27475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est2:C27475
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                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
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JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                ORIGIN
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/tissue_type="root tips"
/dev.stage="harvested after 3 days of N-starvation"
/dev.stage="harvested after 3 days of N-starvation"
/dev.stage="harvested after 5 site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapXR vector from
Stratagene and packaged using Giapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using ExAssit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicago truncatula
sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL369357 399 bp mRNA EST 03-AUG-2000 MtBA30E09F1 MtBA Medicago truncatula cDNA clone MtBA30E09 T3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Bm 191 91006 EVRX cedex - France
Email: seqref@enoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 399)
Journet, E. Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Glaninazzi-Pearson, V. and Gamas, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula ESTs from nitrogen-starved roots Unpublished (2000)
                                                                                                                                                                                                                                                                                                                     Length: 17
Gaps: 0
Percent Identity: 94.118
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1. 399
/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="texon:3880"
/clone="MtBA30E09"
                                                                                                                                                                                                                                                   Align seg 1/1 to: C27475 from: 1 to: 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL369357
AL369357.1 GI:9669110
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                                        Ratio: 4.588
Percent Similarity: 100.000
                                                                                                                                                                                US-09-485-529-104 x C27475
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alignment_scores:

alignment_scores:

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seq_name: gb_est1:AL369482
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryzae.

E (bases 1 to 399)
S saski, T. and Yamamoto, K.

Rice cDNA from immature leaf including apical meristem (2000)
Unpublished (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AU091413 399 bp mRNA EST 05-JUN-2000
DEFINITION AU091413 Rice cDNA from immature leaf including apical meristem (under short day condition) Oryza sativa cDNA clone E60220, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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Percent Identity: 94.118
               Gaps: 0
Percent Identity: 94.118
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                                                                                                                      to: 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Nipponbare"
/db_xref="taxon:4530"
/clone="E60220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                    to: AL369357 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                           AU091413.1 GI:8251089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 81-298-38-7468
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US-09-485-529-104 x AU091413
                                                                                 US-09-485-529-104 x AL369357
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Percent Similarity: 100.000
               Ratio: 4.588
Percent Similarity: 100.000
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78.00
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Quality:
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SOURCE
ORGANISM
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/Listue__rype__root_lister 3 days of N-starvation"
/dev_stage="harvested affer 3 days of N-starvation"
/note="Vector: pBluescript pSK; Site_]: EcoRi; Site_2:
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapKR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using ExAssit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, ENTY, France)."
                                                                                                                                                                                                                          Medicago truncatula
bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
AL369\overline{4}82 458 bp mRNA EST 03-AUG-2000 MtBA31D06F1 MtBA Medicago truncatula cDNA clone MtBA31D06 T3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                   Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson, V. and Gamas, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biologie Moleculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 31226 Castanet-Tolosan Cedex, France (Email Mt-est@toulouse.inra.fr Website: http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicago truncatula ESTs from nitrogen-starved roots Unpublished (2000)
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Gaps: 0
Percent Identity: 94.118
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BP 191 91006 EVRY cedex - France
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/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBa31D06"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="MtBA"
/tissue_type="root tips"
                                                                                                                          AL369482.1 GI:9669235
                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 458)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
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US-09-485-529-104 x AL369482
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Percent Similarity: 100.000
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Ratio:
                                                                     sequence.
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us-09-485-529-104.p2n.rst

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seq_name: gb_est1:AU222715
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AUTHORS
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KEYWORDS
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                  AL371425 466 bp mrwa
MtBA44B05F1 MtBA Medicago truncatula cDNA clone MtBA44B05 T3, mRNA
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Contact : Pascal Games and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-estétoulouse.inra.fr Website : http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 466)
Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson
, V. and Gamas, P.
                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula ESTs from nitrogen-starved roots Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cultivar="Jemalong"
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/clone_lib="MtBA"
                                                                                                                                                                                    AL371425.1 GI:9671178
                                                                                                                                                                                                                                      Medicago truncatula
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US-09-485-529-104 x AL371425
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Percent Similarity: 100.000
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                                                                seq_name: gb_est1:AL371425
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                                                                                                 seq_documentation_block:
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Ratio:
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                               323 T 323
17 a 17
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ORIGIN
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KEYWORDS
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Lotus japonicus.
Cutus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
seq_documentation_block: 467 bp mRNA EST 30-JUL-2001 LOCUS AU222715 467 bp mRNA clone S0583, mRNA sequence. DEFINITION AU222715 Rice shoot Oryza sativa cDNA clone S0583, mRNA sequence. ACCESSION AU222715
                                                                                                                                                                                                                                                                              1 (bases 1 to 467)
Sasaki, T. and Yamamoto, K.
Sasaki, T. and Yamamoto, K.
Sicon at tolated shoot (2001)
Unpublished (2001)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
Tel: 81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV422153 484 bp mRNA EST 23-MAY-2000 AV422153 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM005b04_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     days old)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 94.118
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/note="Etiolated shoot (8
136 c 176 g 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AU222715 from: 1 to: 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                  AU222715.1 GI:15008327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="S0583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 81-298-38-7468
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US-09-485-529-104 x AU222715
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Percent Similarity: 100.000
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                                                                                                                                                         Oryza sativa.
Oryza sativa
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/db_xref="taxon:3880"
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Percent Similarity: 100.000
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barrel medic.
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LOCUS AW695914
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SOURCE
ORGANISM
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VERSION
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                                                                                                                                                                Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
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/note="Yoctor: pBluescriptII SK-; Site_1: EcoRI; Site_2:
Xhoi; isolate=Miyakojima M0-20" 。
144 c 103 g 107 t
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He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Dixon
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On Apr 14, 2000 this sequence version replaced gi:7572088.
Contact: Dixon RA
l (bases 1 to 484)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NF117E10ST1F1082 Developing stem Medicago truncatula cDNA clone NF117E10ST 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
1510 San 17302
Fax: 580 221 7380
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Percent Identity: 94.118
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EST.
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Percent Similarity: 100.000
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KEYWORDS
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Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bel
,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
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Unpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7570676.
Contact: Dixon RA
                                                                                                                                                                                                                                                                             /dev_stage="Pooled developmental"
/note="Vector: Lambda Lap; Contains a mixture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 17
Gaps: 0
Percent Identity: 94.118
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                                                                                                                      1. 537
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/db_xref="taxon:3880"
/clone="NF17E1085"
/clone_lib="Developing stem"
Email: radixon@noble.org
Insert Length: 686 Std Error: 0.00
Plate: 117 row: E column: 10
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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Insert Length: 654 Std Error: 0.00
Plate: 099 row: H column: 09
Seg primer: TCACACAGGAAACAGCTATGAC.
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7302
Fax: 580 221 7380
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                                                                                                                                                                                                                                                                                                                                     internodal stem segments"
120 c 87 g 131
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                                                                                                                                                                                                                                                        /tissue_type="stem"
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us-09-485-529-104.p2n.rst

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144 C
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US-09-485-529-104 x BI308816
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Ratio: 4.588
Percent Similarity: 100.000
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
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J. and Fraser, C.M.
J. and Fraser, C.M.
ESTS from developing reproductive tissues of Medicago truncatula Unpublished (2001)
Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Fax: 713-798-7078
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/dev_stage="Immature pods, ranging in age from 15 to 30
days after pollination"
/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
EcoRI; EcoR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI308816 614 bp mRNA EST 20-JUL-2001
EST530226 GPOD Medicago truncatula cDNA clone pGPOD-8H2 5' end,
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/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
121 c 83 g 158 t
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More information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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Percent Identity: 94.118

    .614
/organism-"Medicago truncatula"
/cultivar-"A17"

/clone-"NF099H09ST"
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B395671e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-485-529-104 x AW695914
                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 4.588
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AW695914
                                                                                                                                                                                                                                                                                                                                                                             78.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BI308816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est2:BI308816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS BI308816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicago.
                                                                                                                                                                                                                                                                                                                                             alignment_scores:
Quality:
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KEYWORDS
SOURCE
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JOURNAL
COMMENT
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in liquid nitrogen. Pod walls were pooled for mRNA extraction. CDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into the Unisap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper hade and propogated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
isolated pod walls were collected and immediately frozen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 655)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW694061 655 bp mRNA EST 15-JUN-2000 NF072A05ST1F1036 Developing stem Medicago truncatula cDNA clone NP072A05ST 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 GACGAGTTGTTAGCAGCATTAGGTTACAAGGTTCGCTCTTCCGACATGGC 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7302
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .655
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NFO72A05ST"
/clone=lib="Developing stem"
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Insert Length: 655 Std Error: 0.00
Plate: 072 row: A column: 05
Seq primer: TCACACAGAAACAGCTATGAC.
Location/Qualifiers
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Unpublished (2000)
Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 g
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from: 1 to: 656
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US-09-485-529-104 x AW696350
US-09-485-529-104 x AW694064
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                                   to: AW694064
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                                                                                                                                                                                                               seq_name: gb_est1:AW696350
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                                                                                                                                                                                                                                                 seq_documentation_block:
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Ratio:
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                                   Align seg 1/1
                                                                                                                                                                          355 T 355
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Darrel medic.
Medicago truncatula
Medicago truncatula
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Mosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolleae;
Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 656)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Mombulished (2000)
Contact: Dixon RA Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                             AW694064 656 bp mRNA EST 15-JUN-2000 NF072A07STIF1052 Developing stem Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="stem"
/dev_stage="Pooled developmental"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
145 c 107 g 166 t
                                                                                                                                                                                                                            Leugth: 17
Gaps: 0
Percent Identity: 94.118
                                                                                   Gaps: 0
Percent Identity: 94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .656
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF072A0757"
/clone_lib="Developing stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: radixonenoble.org
Insert Length: 656 Std Error: 0.00
Plate: 072 row: A column: 07
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                             to: 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NF072A07ST 5', mRNA sequence.
                                                                                                                                                                                           Align seg 1/1 to: AW694061 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW694064
AW694064.1 GI:7568801
                                                                                                                                                          US-09-485-529-104 x AW694061
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Ratio: 4.588
Percent Similarity: 100.000
                                                                                   Ratio: 4.588
Percent Similarity: 100.000
                                                                    78.00
                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est1:AW694064
                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AW694064
                                                                      Quality:
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                                                   alignment_scores:
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                                                                                                                                           alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                                        348 T 348
                                                                                                                                                                                                                                                                                                     17 a 17
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VERSION
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SOURCE
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ORIGIN
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Medicago truncatula
Medrayota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae;
                                                                                                                                                                                                                                                                                                          1 (bases 1 to 667)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Unpublished (2000)
AW696350 667 bp mRNA EST 15-JUN-2000 NF107A12ST1F1088 Developing stem Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="stem"
/dev.stage="Pooled developmental"
/dev.stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Tel: SB0 221 7380
Fax: 580 221 7380
Email: radixon@noble.org
Email: radixon@noble.org
Plate: 107 row: A column: 12
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 17
Gaps: 0
Percent Identity: 94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Medicago truncatula",
/db_xrsf="traxon:3880"
/clone="NRIO7A12ST"
/clone_lib="Developing stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 667
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147 c 126 g 16
                                             NF107A12ST 5', mRNA sequence.
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1..667
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                                                                                                   AW696350.1 GI:7571200
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367 T 367

304 T 304

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Ratio: 4.588
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               available at 'h
Seg primer: T3.
     seq_name: gb_est1:AW584661
                                                     seq_documentation_block:
LOCUS AW584661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_itype="roots colonized with Glomus versiforme"
/tissue_itype="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
/lab_host="E. coli strain XLOLR"
/note="vector: pBluescript SR.; site_1: ECORI; Site_2:
Xho1; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cellis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Medicago truncatula/Glomus versiforme mixed EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 580-221-7380
Email: mjharrison@noble.org
Other name: MHAM-2c-H09; Date: 3/14/00; Updated to the Database of
Expressed Sequence Tags (dbEST) on 04/27/00; More information is
available at 'http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                               Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library.
Eukaryota: mixed EST libraries.
I (bases 1 to 68 3)
Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D.,
Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
ESTS from roots of Medicago truncatula after colonization with
                                          AW584593 683 bp mRNA EST 07-SEP-2000 N210669e MHAM Medicago truncatula/Glomus versiforme mixed EST aW584593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="MHAM-2P17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 94.118
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                        Glomus versiforme
Unpublished (2000)
Contact: Harrison M.J.
                                                                                                                                                                      AW584593.1 GI:7261647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 4.588
Percent Similarity: 100.000
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US-09-485-529-104 x AW584593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 683
seq_name: gb_estl:AW584593
                                                Quality:
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                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                DEFINITION
                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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FEATURES

TITLE

COMMENT

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/organism="Medicago truncatula/Glomus versiforme mixed EST
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//note="Vector: phluescript SK-; Site_1: EcoRI; Site_2:
Xhor; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
firstionality ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: miharrison@noble.org
Other name: MHAM-2d-H09; Date: 3/14/00; Updated to the Database of
Expressed Sequence Tags (dbEST) on 04/27/00; More information is
available at http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="roots colonized with Glomus versiforme" Adev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-incoulation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
                                                                                                                                                                                                               Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.
I (bases I to 701)
Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D.,
Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
ESTS from roots of Medicago truncatula after colonization with
AW584_661 701 bp mRNA EST 07-SEP-2000 N210765e MHAM Medicago truncatula/Glomus versiforme mixed EST library CDNA clone MHAM-2P18, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /colitivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="MHAM-2P18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 GACGAGTIGITIAGCAGCATTAGGTTACAAGGTTCGCTCTTCCGACATGGC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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Gaps: 0
Percent Identity: 94.118
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                                                                                                                                                AW584661.1 GI:7261715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Harrison M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-485-529-104 x AW584661
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17 a 17

17 a 17

to: 683

from: 1

Align seg 1/1 to: AW584593

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

DEFINITION

ACCESSION

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/clone_lib="Hood"
/clone_lib="Hood"
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/dev_stage="24 hours after treatment in the dark at 26 C
/dev_stage="24 hours after treatment in the dark at 26 C
/dev_stage="24 hours after treatment in the dark at 26 C
/dev_stage="26 hours after after at 26 C
/dev_stage="26 hours after at 26 hou
                                                                                                                                                                                                                                                                                                                                 Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Rosidae, eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae,
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LOCUS BG440209 684 bp mRNA EST 15-MAR-2001
DEFINITION GA__Ea0006G06f Gossypium arboreum 7-10 dpa fiber library Gossypium
EST508687 HOGA Medicago truncatula cDNA clone pHOGA-15H23 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from the recombinant lambda-žap phage using Ex-assist helper phage and propagated in SOLR cells." 170 c 131 g 186 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 706-542-4457
Fax: 706-542-4412
Email: hahm@corc.uga.edu
1390674e TIGR sequence name: MTMBU48TK More information is available at: www.medicago.org
seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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Percent Identity: 94.118
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220 Riverbend Road, Athens, GA 30602-4712,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
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/db_xref="taxon:3880"
/clone="pHOGA-15H23"
                                                         mRNA sequence.
BG647068
BG647068.1 GI:13782180
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US-09-485-529-104 x BG647068
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Percent Similarity: 100.000
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     DEFINITION
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//tissue_type="2-3 day old seedlings"
//dev_stage="2-3 day old seedlings"
//note="Organ: Root; Vector: pBK-CMV; Site_1: ECORI;
//note="Organ: Root; Vector: pBK-CMV; Site_1: ECORI;
//tissue_type="Root hairs" (30% w/w) and 2-3cm root tips
//tissue_type="Root hairs" (30% w/w) and filed, and
//tissue_type="Root hairs" (30% w/w) and hairs (30% w/w)
//tissue_type="Root hairs" (30% w/w) and hairs
//tissue_type="Root hairs" (30% w/w)
//tissue_type="Root 
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Department of Biological Sciences and Howard Hughes Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 719)
Covitz, P.A., Smith, L.S. and Long, S.R.
Expressed sequence tags from a root-hair-enriched medicago
                                                                                                                                                                                                                                                                                                                                       AA660952 719 bp mRNA EST 08-M.
00849 MtRHE Medicago truncatula cDNA 5', mRNA sequence
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Gaps: 0
Percent Identity: 94.118
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Gilbert Biology, Stanford, CA 94305-5020,
121 650 723 323
Fax: 650 725 8309
Email: fa.srl@forsythe.stanford.edu
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/organism="Medicago truncatula"
/cultivar="Jemalong"
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Plant Physiol. 117 (4), 1325-1332 (1998)
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/clone_lib="MtRHE"
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Percent Similarity: 100.000
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US-09-485-529-104 x AA660952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est2:BG647068
                                                                                                                                                                seq_name: gb_est1:AA660952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          barrel medic.
                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AA660952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS BG647068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA660952
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                                                   367 T 367
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source

FEATURES

BASE COUNT ORIGIN

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ESTs from roots of Medicago truncatula after colonization with
                     Glomus versiforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est1:AW688657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medicago.
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ORGANISM
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                                        JOURNAL
                                                                                                                                                                                                                                                                                         FEATURES
  TITLE
                                                           COMMENT
                                                                                                                                                                                                    Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

an integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D.,
Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:29729"
/clone="GA_Ea0006G06f"
/clone_lib="GASSypium arboreum 7-10 dpa fiber library"
/tlssue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW584411 712 bp mRNA EST 07-SEP-2000 N210477e MHAM Medicago truncatula/Glomus versiforme mixed EST library cDNA clone MHAM-2017, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
145 c 138 g 196 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST library
EST library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 GACGAGTTATTAGCTGTTTTGGGTTACAAAGTTCGGTCATCAGATATGGC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
arboreum cDNA clone GA_Ea0006G06f, mRNA sequence.
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1 (bases 1 to 712)

Harrison, M.J., Liu, J., Peng, H., Gonzales, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 17
Gaps: 0
Percent Identity: 88.235
                                                                                                                                                                                                                                                                                                                                            Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Gossypium arboreum"
/strain="AKA"
                                                                                                                                                                                                                                                                                                          Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 684
                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 682.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host-"E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar-"8400"
                                        BG440209.1 GI:13349859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW584431.1 GI:7261485
                                                                                 Gossypium arboreum
                                                                                                  Gossypium arboreum
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VERSION
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ORIGIN
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KEYWORDS
SOURCE
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                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                     JOURNAL
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                                                                                                                                                                                                                                               TITLE
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/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-incollation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
/note="vector: pBluescript SK; Site_1: Ecorl; Site_2:
/note="vector: pBluescript SK; Site_1: Ecorl; Site_2:
XNOI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-incollation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gloapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .712
/organism="Medicago truncatula/Glomus versiforme mixed EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
The: S80-221-3580
Email: mjharrison@noble.org
Other name: MHAM-2a-H09; Date: 3/14/00; Updated to the Database of
Expressed Sequence Tags (dbEST) on 04/27/00; More information is
available at 'http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AM688657 651 bp mRNA EST 15-JUN-2000
DEFINITION NFOLOBOASTH1000 Developing stem Medicago truncatula cDNA clone
NFOLOBO4ST 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cultivar="Medicago truncatula genotype Al7"
/db_xref="taxon:119092"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 17
Gaps: 0
Percent Identity: 88.235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone-"MHAM-2017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="MHAM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW688657.1 GI:7563393
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US-09-485-529-104 x AW584431
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Percent Similarity: 100.000
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 a 17
                                                                                                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS A1495884 311 bp mRNA EST 01-DEC-1999
DEFINITION Sb17d07.y1 Gm-c1004 Glycine max CDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1004-9062 5' similar to TR:023643 023643 RGA2 PROTEIN. [1] ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shoemaker, R., Kelin, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                     He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                        Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /close_lib="Developing stem"
/tissue_type="stem"
/dev_stage="pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
139 c 143 g 175 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                Unpublished (2000)
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 0
Percent Identity: 93.750
                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                              Email: radixon@noble.org
Insert Length: 651 Std Error: 0.00
Plate: 010 row: B column: 04
Seq primer: TCACACAGGAAACACTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 651
                                                                                                                  Medicago truncatula stem library
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:3880"
/clone="NF010B04ST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AW688657 from: 1
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US-09-485-529-104 x AW688657
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Percent Similarity: 100.000
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REFERENCE
                       AUTHORS
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/note="Vector: palescript II XR; Site_1: ECORI; Site_2: XhoI; Root cDNA. The mRNA was isolated from entire roots of 8 day old "Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA synthesis Kit (catalog #200401) was used to synthesize the CDNA. First- strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated.

Stratagene's first-strand synthesis primer was used [GAGGAGAGAGAGAGACATCTCGAG(T).18]. After second-strand synthesis, the CDNA ends were 'polished' with clone Ptu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI, all XhoI sites in the CDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using dibcobRL Life size-fractionated with a 500bp cutoff, using dibcobRL Life Technologies' CDNA size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that had been digested with ECORI and ANDI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with CDNA inserts. Blue colonies 90-15) have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Coryell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University, Flagstaff, Az 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, emall: paul.keim@nau.edu, virginia.coryellFanu.edu" 74 e 88 g 62 t
                                                                                                                                                                                    Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com Seq primer: -40RP from Gibco
                                                                                                                Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Glycine max"
/db_xxref="taxon:8847"
/clone="EBNOME SYSTEMS CLONE ID: Gm-cl004-9062"
/clone_lib="'Gm-cl004"
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Gaps: 0
Percent Identity: 82.353
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Location/Qualifiers
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/lab_host="XL10-Gold"
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US-09-485-529-104 x AI495884
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Percent Similarity: 100.000
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Washington University School of Medicine,
    Agriculture and Agri-Food Canada
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Spermatophyta, Magnollophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                                  The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 153-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Loteae;
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/organism="Lotus japonicus"
/db_xref="taxon:340s"
/db_xref="taxon:340s"
/clone="wML061all_r"
/clone="tayoung plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="tayoung plants (two-week old)"
/note="Vector: pBluescriptII S; site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
a 95 c 102 g 62 t
                                                                                                                                                                                                             1 (bases 1 to 365)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from legume. Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
    23-MAY-2000
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                    AV409731 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWL061e11_r 5', mRNA sequence.
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Harris,N., Chapman,B.P. and Gijzen,M.
Gene expression in developing soybean seed coats
Unpublished (2000)
Contact: Gijzen M
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Percent Identity: 82.353
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Locus BE659954 455 bp mRNA EST
DEFINITION 746 GmaxSC Glycine max cDNA, mRNA sequence.
ACCESSION BE659954
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      mRNA
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                                                                              AV409731.1 GI:7722585
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365 bp
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US-09-485-529-104 x AV409731
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Percent Similarity: 100.000
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                                                                                                                      Lotus japonicus.
Lotus japonicus
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/tissue_tipe="Seed coats"
/tissue_tipe="Seed coats"
/lab_host="E. coli strain XLOLR"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBK-CWY, Site=1: EcoRI; Site=2: XhoI; This cDMA library was constructed from polyA+ enriched mRNA from green seed coats in mid to late developemental stage, average fresh weight 250 map per seed. Traces of pod and embryo tissue also present. Complementary DNA was synthesized from mRNA using an XhoI-poly(dT)
linker-primer. EcoRI adopters were lighted to the blunt-ended cDNA fragments and the products were digested with XhoI for directional cloning into lambda ZAP Express vector. This lambda library was amphilited once using E. coli host strain XLI Blue MRF'. Inserts were then subcloned by mass excision using Exassist helper phage for conversion into phagemid vector pBK-CMV in E. coli host

        seq_documentation_block:
        465 bp
        mRNA
        EST
        28-NOV-2000

        LOCUS
        BF424878
        465 bp
        mRNA
        CRCONG INCOME SYSTEMS. CLONE ID:

        DEFINITION su52b08.yl Gm-c1069 Glycine max cDNA clone GENOME SYSTEMS. CLONE ID:
        Gm-c1069-471 5' similar to TR:023642 023642 RGA1 PROTEIN. [1] ;,

        ACCESSION
        BF424878

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1391 Sandford Street, London, Ontario, Canada N5V 4T3
Tel: 519 457 1470
Fax: 519 457 397
Email: gijzenméem.agr.ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 others
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/organism="Glycine max"
/cultivar="Harosoy 63"
/db_xref="taxon:3847"
/clone_llb="GmaxSC"
                                                                                                                                               Location/Qualifiers
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US-09-485-529-104 x BE659954
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Percent Similarity: 100.000
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    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript II SK+; Site_I: EcoRI; Site_2:
XhoI; The CDNA library was constructed from mRNA isolated
from degenerating cotyledons of 9-10 day old etholated
seedlings for the cultivar Williams. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments
were transformed into DHIOB host cells (GibcoBR). This
library was constructed in the laboratory of Dr. Randy
                                                       Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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Colebatch,G., Freund,S., Trevaskis,B and Udvardi,M.
Lotus japonicus root nodule ESTs: tools for functional genomics
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-2000
                                                                                                                                                                                                                                                                                                                                        /tissue_type="Degenerating cotyledons, 9-10 day old etiolated seedling" /lab_host="DH10B"
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                 /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1069-471"
/clone_lib="Gm-c1069"
                                                                                                                                                                   info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 412.
Location/Qualifiers
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Gaps: 0
Percent Identity: 82.353
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314 286 1810
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US-09-485-$29-104 x BF424878
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Lotus japonicus
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Ratio:
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LINESTATELL JOSU DE MKNA EST 15-AUG-2001
LINESTATELL LOTUS Japonicus nodule library 5 and 7 week-old Lotus
Japonicus CDNA 5', mRNA sequence.
BI419686.1 GI:15190709
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="5 and 7 week-old plants"
//dev_stage="5 and 7 week-old plants"
//note="Organ: Nodule; Vector: pSPORT1; Site_1: SalI;
Site_2: NotI; The library was prepared using mRNA
extracted from nodules of 5 and 7 week-old Lotus plants.
Nodules were induced by, and contained Mesorhizobium
strain_R7A."
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Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Lotus japonicus root nodule ESTs: tools for functional genomics
Unpublished (2000)
Contact: Udvardi MK
                                                                                                                                                                                                                                           /organism="Lotus japonicus"
/cultivar="Gifu (B-129)"
/db_xref="taxon:34305"
/clone_lib="Lotus japonicus nodule library 5 and
week-old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Udvardi MK
Molecular Plant Nutrition
Max Planck Institute of Molecular Plant Physiology
Am Muchlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
Email: udvardi@mpimp-golm.mpg.de
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Max Planck Institute of Molecular Plant Physiology
Am Muchlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
Email: udvardi@mpimp-golm.mpg.de
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Gaps: 0
Percent Identity: 82,353
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High quality sequence stop: 478.
Location/Qualifiers
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Location/Qualifiers
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Percent Similarity: 100.000
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LOCUS B1419686
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'tissue_type="roots infected with Phytophthora
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                        medicaginis
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Fax: 517 353 9334
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Ratio:
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Fedorova, M., Plerson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S., Peng, H. Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
ESTs from roots of Medicago truncatula after inoculation with Phytophthora medicaginis
Compublished (1999)
Contact: Carroll P. Vance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                /note="Organ: Nodule; Vector: pSPORT1; Site_1: SalI; Site_2: NotI: The library was prepared using mRNA extracted from nodules of 5 and 7 week-old Lotus plants. Nodules were induced by, and contained Mesorhizobium strain R7A."
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Tel: 612 625 5715
Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW267879 587 bp mRNA EST 07-SEP-2000 EST306157 DSIR Medicago truncatula cDNA clone pDSIR-8K8, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: vance004@maroon.tc.umn.edu
Minnesota EST name:M250388e
TIGR sequence name:WTBAF64TK
More information, including clone ordering, is available at.
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                /clone_lib="Lotus japonicus nodule library 5 and 7 week-old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="5 and 7 week-old plants"
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Gaps: 0
Percent Identity: 82,353
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/cultivar-"genotype A17"
/db_xref="taxon:3880"
/clone-"pDSIR-6K8"
/clone_lib="DSIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 586
/cultivar="Gifu (B-129)"
/db_xref="taxon:34305"
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Medicago truncatula
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US-09-485-529-104 x BI419686
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Percent Similarity: 100.000
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Alea Stage="roots harvested at 10 days post inoculation with Phytophthora medicaginis"

Alab_host="b. coli strain XLOLR"

Anote="vector: peluescript SK-; Site_1: EcoRI; Site_2:

XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10 days post inoculation with Phytophthora medicaginis. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells. Note: EST may be of fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
614292
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 374)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de
Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
Anew set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS BE524828 374 bp mRNA EST 19-MAR-2001
DEFINITION M54G7STW Arabidopsis developing seed Arabidopsis thallana CDNA
Clone M54G7 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GACGAGTTGTTAGCAGCATTAGGTTACAAGGTTCTCTTCCGACATGGC 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 17
Gaps: 0
Percent Identity: 88.235
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Dept. of Biochemistry & Molecular Biology
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Michigan State University
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alignment_scores:
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ORGANISM
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MEDLINE
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ORIGIN
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TITLE
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KEYWORDS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 457)
Newman, T., deBrulin, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones 95148729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Lambda-PRL2"
//note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mNNA. The mNNA sources were 1) 7
                                                                                                                                  /note="Organ: Developing seed; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoII" 88 c 87 g 102 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T22782 457 bp mRNA EST 06-NOV-1997
4790 Lambda-PRL2 Arabidopsis thaliana cDNA clone 107E8T7, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Thomas Newman
MSU-DDE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Nov 6, 1997 this sequence version replaced gi:932620
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3702"
/clone="M54G7"
/clone_lib="Arabidopsis developing seed"
                                                                          /tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.col1"
                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 82.353
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Strain="var columbia"
/db_xref="taxon:3702"
/clone="107E8T7"
                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: BE524828 from: 1 to: 374
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Seq primer: T7 dye primer.
Location/Qualifiers
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       r22782.
T22782.1 GI:2597312
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US-09-485-529-104 x BE524828
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                                                                                                                                                                                                                                                                                            Ratio: 4.118
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                           70.00
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SOURCE
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Arabidopsis thallana
Arabidopsis thallana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 545)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Arabidopsis thaliana aboveground organs two to
              grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using 011go dT primed cONA.

86 c 87 g 125 t 18 others
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV526467 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana cDNA clone AP214e05R 5', mRNA sequence. AV526467 GI:8685995
day germinated etiolated seedlings; 2) tissue culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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Gaps: 0
Percent Identity: 82.353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/clone="AP214e05R"
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Ratio: 4.118
Percent Similarity: 100.000
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US-09-485-529-104 x T22782
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LOCUS AV526467
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195 GATGAGCTTTTGGCGTTTTGGGTTACAAGGTCAAAACTTCAGACATGGC 244
                                                                                                                              seq_name: gb_est2:BI267918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosida II; Malvales; Malvaceae; Gossyplum.

1 (bases 1 to 655)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

M. integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="GA_Ea0018120f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /jab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
188 c 132 g 170 t
                                                                                                                                                                                                 188 GATGAGCTTCTTGCTGTTCTTGGCTACAAGGTTCGATTCTTCTGAGATGGC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AspGluLeuLeuAlaAlaLeuGlyTyrLySValArgAlaSerAspMetAl 17
                                                                                                                                                                         1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                    Percent Identity: 82.353
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/organism="Gossypium arboreum".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 647.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="8400"
/db_xref="taxon:29729"
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US-09-485-529-104 x BG442853
                                                                                    US-09-485-529-104 x AV526467
  Ratio: 4.118
Percent Similarity: 100.000
                                                                                                                              Align seg 1/1 to: AV526467
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Ratio: 4.118
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est2:BG442853
                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
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                                                                alignment_block
                                                                                                                                                                                                                                                                                                   238 T 238
                                                                                                                                                                                                                                                           17 a 17
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
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/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="Ne112E071N"
/clone=lib="Insect herbivory"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

were harvested and pooled. 2 others
                                                                                                                                                                                                                                                                                                                  Medicago.

1 (bases 1 to 227)

Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores, H.R., Imman,J.T., Weller,J.W. and May,G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Rosidae, eurosids I; Fabales, Fabaceae; Papilionoideae, Trifolieae,
                        BI267918 227 bp mRNA EST 18-JUL-2001
NF112E07IN1F1055 Insect herbivory Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 17
Gaps: 0
Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: kkorth@comp.uark.edu
Insert Length: 27 Std Error: 0.00
Plate: 112 row: E column: 07
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 227
                                                                         NF112E07IN 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: BI267918 from: 1
                                                                                                        BI267918
BI267918.1 GI:14873367
                                                                                                                                                                                                                  Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-485-529-104 x BI267918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 4.000
Percent Similarity: 100.000
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seq_documentation_block:
LOCUS B1267918
                                                                                                                                                                                    barrel medic.
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Ratio:
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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/clone_lbb="MtbA"
/clone_lbb="MtbA"
/tissue_type="root tips"
/tissue_type="root tips"
/dev_stage="harvested after 3 days of N-starvation"
/dev_stage="harvested after 3 bays of N-starvation"
/note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). CDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapxR vector from
Stratagene and packaged using Giapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using ExAssit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
                             Medicago truncatula
bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS.INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-est@toulouse.inra.fr Website:
                                                                                                                                        Medicago.

1 (bases 1 to 398)

Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson, V. and Gamas, P.
Medicago truncatula ESTs from nitrogen-starved roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI267177 442 bp mRNA EST 18-JUL-2001
NF102E07IN1F1055 Insect herbivory Medicago truncatula cDNA clone
NF102E07IN 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://sequence.toulouse.inra.fr/Mtruncatula.html).
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 0
Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone-"MtBA44A11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI267177
BI267177.1 GI:14871977
                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-485-529-104 x AL371416
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Percent Similarity: 100.000
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barrel medic.
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LOCUS BI267177
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                             ORGANISM
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JOURNAL
COMMENT
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                                                                                                                                                                                                AUTHORS
                                                                                                                                                                     REFERENCE
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KEYWORDS
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     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                 Torres-Jerez, I to 288)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
Unpublished (2000)
On Jul 14, 2000 this sequence version replaced gi:9191308.
                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Kosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolleae; Medicago.
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                                                    BE317531 288 bp mRNA EST 21-DEC-2000 NF051B06LF1F1045 Developing leaf Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of very
young, developing, mature and senescing leaves."
34  77  9  70  t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: gdmay@noble.org
Medicago Genome Initiative accession: MGI:S:21598
Insert Length: 766 Std Error: 0.00
Plate: 051 row: B column: 06
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 0
Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NFO51B06LF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
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                                                                                                           NF051B06LF 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                   BE317531.2 GI:11961937
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AL371416.1 GI:9671169
EST.
                                                                                                                                                                                                                                                       Medicago truncatula
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US-09-485-529-104 x BE317531
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Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: May GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est1:AL371416
                          seq_documentation_block:
LOCUS BE317531
DEFINITION NF051B06LF1F1
                                                                                                                                                                                                                          barrel medic.
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Ratio:
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source

FEATURES

BASE COUNT ORIGIN

DEFINITION

ACCESSION

VERSION KEYWORDS

SOURCE

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Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
2510 Sam Noble Perkway, Ardmore, OK 73402, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                    truncatula"
                                                                                                                                                                                    2510 Sam North 251 7391 Tel: 580 221 7390 Fax: 580 221 7380 Email: gdmay@noble.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                         Insert Length: 454 Std Error: 0.0
Plate: 084 row: H column: 12
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Plantlets"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago truncatula stem library
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Medicago tr
/db_xref="taxon:3880"
/clone="NF084H12DT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Drought"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
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Percent Similarity: 100.000
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US-09-485-529-104 x BF634231
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="Ne102071N"
/clone="Ne102071N"
/clone="lb="Insect herbivory"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

54 a 81 c 93 g 112 t 2 others
                                                                                                                                  Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
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Medicago truncatula
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS BF634231 454 bp mRNA EST 19-DEC-2000 DEFINITION NF084H12DT1F1103 Drought Medicago truncatula cDNA clone NF084H12DT
                                                                                                                                                                                                                                                                Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 0
Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                    Email: kkorthecomp.uark.edu
Insert Length: 442 Std Error: 0.00
Plate: 102 row: E column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: BI267177 from: 1 to: 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                Medicago truncatula
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                                                                                                                                                                                                                                                    Unpublished (2000)
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ACCESSION | BF634231
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Percent Similarity: 100.000
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US-09-485-529-104 x BI267177
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      barrel medic.
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LOCUS
BF634231
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                                                                                                                                         REFERENCE
                                                                                                                                                             AUTHORS
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FEATURES

TITLE

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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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1 (bases 1 to 470)

1 (bases 1 to 470)

2 (bases 1 to 470)

3 (bases 1 to 470)

4 (bases 1 to 470)

5 (bases 1 to 470)

6 (bases 1 to 470)

7 (bases 1 to 470)

7 (bases 1 to 470)

8 (bases 1 to 470)

8 (bases 1 to 470)

9 (bases 1 to 4
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On Apr 14, 2000 this sequence version replaced gi:7566005.
Contact: Dixon RA
                                                                                                                                             1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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"Jab_host="E. coli strain XLOLR"

//Jab_host="E. coli strain XLOLR"

//Jab_host="Vector: pBluescript SK -: Site_1: EcoRI; Site_2:

//Anoi. colnA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

9 6 c 106 g 123 t
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Vandenbosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
                                                                                                                                                                                        /tissue_type="Seedling roots"
/dev_stage="24 hours post-inoculation with Sinorhizobium
meliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE205231 495 bp mRNA EST 05-SEP-2000
EST397907 KVO Medicago truncatula CDNA clone pKVO-21C7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESTs from uninoculated seedling roots of Medicago truncatula Unpublished (1999)
Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 GATGAACTCTTAGCTGTAGTTGGTTACAAAGTGAAATCTTCAGACATGGC 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 76.471
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualiflers
                                                             /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pkV1-2B16"
/clone=lib="kV1"
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Tel: 409 845 7707
Fax: 409 845 2891
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Texas A&W University name:T265003e
TIGR sequence name:MTGBK16TK
More information is available at.
http://chrysie.tamu.edu/medicago
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Texas A&M University
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Ratio: 4.000
Percent Similarity: 100.000
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US-09-485-529-104 x BE202661
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Rakaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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AndenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESTs from roots of Medicago truncatula 24 hours after inoculation with Sinorilizobium meliloti Unpublished (1999)
Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-2000
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EST402683 KV1 Medicago truncatula cDNA clone pKV1-2B16, mRNA
                                                                                                                                                                                                                               /organism="Medicago truncatula"
/db_xref="taxon:3880"
/db_xref="taxon:3880"
/clone="NF03960157"
/clone=lib=beveloping stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
1 98 c 98 g 123 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA 1510 San 1521 7302 Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 17
Gaps: 0
Percent Identity: 76.471
                                                                                        Email: radixonemoble.org
Insert Length: 678 Std Error: 0.00
Plate: 039 row: G column: 01
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualifiers
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Tel: 409 845 7707
Fax: 409 845 2891
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Texas A&M University.T262354e
TIGR sequence name:MTIADOBTK
More information is available at.
http://chrysie.tamu.edu/medicago
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Texas A&M University
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529-104 x AW691269
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Percent Similarity: 100.000
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/Lissue_trpe="Seedling roots"
//dev_stage="Immediately prior to inoculation with
Sinorhizobium mellioti (0 hour)"
/lab_host="E.coli strain XLOLR"
/lab_host="E.coli strain XLOLR"
/lab_host="E.coli strain XLOLR"
/lab_host="Coli strain XLOLR"
/lab_host="Coli strain XLOLR"
/lab_host="Coli strain XLOLR"
/lab_host="Coli and place from polyA+ enriched RNA. The CDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 544)
Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May
Gonzales, R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May
Medicago truncatula nodulated root library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7317
Fax: 580 221 7380
Email: nlpsivationole.org
Insert Length: 544 Std Error: 0.00
Plate: 018 row: F column: 10
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 76.471
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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/cultivar="genctype A17"
/db_xref="taxon:3880"
/clone="pkV0-21B13"
/clone_lib="KV0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NF018F10NR 5', mRNA sequence.
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Percent Similarity: 100.000
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US-09-485-529-104 x BE205387
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LOCUS AW684591
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                                                                                                                                                           /clone="prv0-21c7"
/clone="prv0-21c7"
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/clone="prv0-21c7"
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/drsue_street = "Coli strain xIOLR"
/drsue_street = "Coli strain xIOLR"
/drsue_street = "Coli strain ying coli proper ying extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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AndenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE205387 522 bp mRNA EST 05-SEP-2000 EST398063 KVO Medicago truncatula cDNA clone pKVO-21B13, mRNA
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  Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                   /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
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Tel: 409 845 7707
Fax: 409 845 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  More information is available at. . http://chrysie.tamu.edu/medicago
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Texas A&M University name:T265159e
TIGR sequence name:MTGBM07TK
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Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE205387
BE205387.1 GI:8748684
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Texas A&M University
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Percent Similarity: 100.000
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US-09-485-529-104 x BE205231
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US-09-485-529-104 x AW693047
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                                                                                                                                        68.00
                                                                                                                                                        4.000
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Ratio:
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KEYWORDS
SOURCE
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                                                                      ORIGIN
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Rakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                Medicago.

1 (bases 1 to 601)

1 (bases 1 to 601)

2 (bases 1 to 601)

3 (bases 1 to 601)

4 (bases 1 to 601)

6 (bases 1 to 601)

7 (bases 1 to 601)

8 (bases 1 to 601)

9 (bases 1 to 601)

9 (bases 1 to 601)

1 (bases 1 to 601)
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On Apt 14, 2000 this sequence version replaced gi:7567783.
Contact: Dixon RA Plant Biology Division
The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7302
Fax: 580 221 7302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NF059C03ST1F1020 Developing stem Medicago truncatula cDNA clone
NF059C03ST 5', mRNA sequence.
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Percent Identity: 76.471
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                                /organism="Medicago truncatula"
/db_xref="taxon:3880"
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/db_xref="taxon:3880"
/clone="NF059C03ST"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: radixonemoble.org
Insert Length: 653 Std Error: 0.00
Plate: 059 row: C column: 03
Seq primer: TCACACAGGAAACACCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                    to: 544
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Location/Qualifiers
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US-09-485-529-104 x AW684591
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Percent Similarity: 100.000
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Medicago truncatula
Eukaryota; Viridiplatatae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW697328 613 bp mRNA EST 21-DEC-2000 NF115E11ST1F1086 Developing stem Medicago truncatula cDNA clone NF115E11ST 5', mRNA sequence.
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                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, US.
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
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barrel medic.
Medicago truncatula
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
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                                                                                                                                                                                                                                             AW690601 620 bp mRNA EST 20-DEC-2000 NF036C12ST1F1000 Developing stem Medicago truncatula cDNA clone NF036C12ST 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 620)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bel
,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
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                         38 GATGAACTCTTAGCTGTAGTTGGTTACAAAGTGAAATCTTCAGACATGGC 87
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
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Percent Identity: 76.471
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AUTHORS
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
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                                                                                                                                                                                                                                                                                                                                                                                                                               AW690574 614 bp mRNA EST 15-JUN-2000
NF031C08ST1F1000 Developing stem Medicago truncatula cDNA clone
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 17
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LOCUS AW690574
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VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

ACCESSION

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FEATURES

JOURNAL COMMENT

TITLE

REFERENCE AUTHORS BASE COUNT ORIGIN

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OM of: US-09-485-529-104 to: Issued_Patents_NA:*
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coda ta 2/1/1na/5A. COMB. seq:195.07-977-414-5+ 30.50 80.55 7.77e+03 2493 coda ta 2/1/1na/5A. COMB. seq:195.07-977-414-5+ 30.50 80.55 7.77e+03 2493 coda ta 2/1/1na/5A. COMB. seq:195.04186 gods 1973-381-5+ 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.04186 gods 1973-381-5+ 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-25+ 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-25+ 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-25+ 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-25+ 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-25+ 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-25+ 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-25+ 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.55 7.77e+03 2495 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.55 7.77e+03 2504 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.55 7.77e+03 2504 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.55 7.77e+03 2504 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.55 7.77e+03 2504 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.55 7.77e+03 2504 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.52 7.77e+03 2504 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.52 7.77e+03 2504 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.52 7.77e+03 2504 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.52 7.77e+03 2504 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.52 7.77e+03 2504 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.52 7.77e+03 2504 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.52 7.77e+03 2504 coda ta 2/1/1na/5A. COMB. seq:195.0418-24- 30.50 80.52 7.77e+03 2504 coda ta

us-09-485-529-104.p2n.rni

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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.00
3.750
80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Michigan
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-981-256A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
                                                                                                                                                                                                                                                                                                                 37 1
1137
                                                                             1074
30.00 87.11 3.3e+0.

+ 30.00 87.11 3.3e-

0.00 86.62 3.5e+03 1.

00 86.62 3.6e+03 1.

00 86.59 3.6e+03 1.

0 86.59 3.6e+03 113

0 86.59 3.6e+03 113

0 86.57 3.6e+03 113

0 86.54 3.6e+03 113

0 86.54 3.6e+03 113

0 86.54 3.6e+03 113
                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
    Sequence 1, Application US/09117853
    Patent No. 6307126
    Sequence 1, Application US/09117853
    Patent No. 6307126
    SENERAL INPORMATION:
    APPLICANT: Hicholas P
    APPLICANT: Beng, Jincong
    APPLICANT: Acrol, Pierre
    APPLICANT: Richards, Donald E
    TITLE OF INVENTION: Nucleic acid encoding GAI gene of Arabidopsis thaliana
    FILE REFERENCE: 620-45
    CURRENT FILING DATE: 1998-08-12
    CURRENT FILING DATE: 1998-08-12
    EARLIER APPLICATION NUMBER: PCT/GB97/00390
    EARLIER APPLICATION NUMBER: PCT/GB97/00390
    EARLIER APPLICATION NUMBER: CB 9602796.6
    EARLIER PILING DATE: 1996-02-12
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 1
    LENGRIH: 1964
    TURNER PILING DATE: 1996-02-12
    SOFTWARE: Patentin Ver. 2.0
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Sequence 4, Application US/08981256A
Sequence 4, Application US/08981256A
Patent No. 6046042
Sequence No. 6046042
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                /cggn__6/prodata/2/ina/PCTUS_COMB.seq:PCT_US94_08326-11 + 30.00
/cggn__6/prodata/2/ina/FCTUS_COMB.seq:US-09-347-819-5 + 30.00
/cggn__6/prodata/2/ina/Fa_COMB.seq:US-08-205-719-1 - 30.00
/cggn__6/prodata/2/ina/Fa_COMB.seq:US-08-746-883-2 - 30.00
/cggn__6/prodata/2/ina/Fa_COMB.seq:US-08-951-924A-1 - 30.00
/cggn__6/prodata/2/ina/Fa_COMB.seq:US-09-172-339-3 - 30.00
/cggn__6/prodata/2/ina/Fa_COMB.seq:US-08-189-256A-10 - 30.00
/cggn__6/prodata/2/ina/Fa_COMB.seq:US-08-189-256A-10 - 30.00
/cggn__6/prodata/2/ina/Fa_COMB.seq:US-08-096-181A-9 + 30.00
/cggn__6/prodata/2/ina/Fa_COMB.seq:US-08-096-181A-9 + 30.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-981-256A-4
                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-117-853-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 0
Percent Identity: 82.353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-09-117-853-1 from: 1 to: 1964
                                                                             /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-096-181A-11 +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-485-529-104 x US-09-117-853-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana US-09-117-853-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 4.118
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Wash:
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 T 337
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APPLICANT: Lahners, Kristine N.
APPLICANT: Rao, Donald D.
TITLE OF INVENTION: @ @3-ADRENERGIC RECEPTOR PROTEIN AND DNA
TITLE OF INVENTION: BKODING SAME
NUMBER OF SEQUENCES: 9
CORRESSEDONDENCE ADDRESS:
ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &
ADDRESSEE: MILTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MILTON
STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390
CITY: Troy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-916-901-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-981-256A-4 from: 1 to: 1078
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           Diskette, 3.5 inch, 1.44 mb
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPUTER: IBM Competible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,256A
FILING DATE: December 22, 1997
CLASSIFICATION: 435
PRIOR APPLICATION OF THE TRY OF THE TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER: 1553-021112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/916,901 FILING DATE: 19920720
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TOWNER: IBM PC COMPALIble
TOWNER: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-485-529-104 x US-08-981-256A-4
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; Sequence 5, Application US/07916901
; Patent No. 5364772
; GENERAL INFORMATION:
APPLICANT: Granneman, James G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
CORRESPONDENCE: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-991-867B-43
                                                                                                                                                                                                                                                                                                                                                                                                         Length: 13
Gaps: 0
Percent Identity: 76.923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: US-07-916-901-5 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floors disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NATA: APPLICATION NAMBER: US/07/991,867B FILING DATE: 12-DEC-1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 Grgtrggcrgcactgggcrccaaggrggggcgrcrgac 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
REGISTRATION NUMBER: 30,955
RECISTRATION NUMBER: 9-324 (WSU)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEG ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICE APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31.794
REFERENCE/DOORET NUMBER: UF114.C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-485-529-104 x US-07-916-901-5/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                      42.00
3.818
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                           NAME/KEY: CDS
; LOCATION: 51..1250
US-07-916-901-5
                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                             TOPOLOGY: 11:7
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: G
STATE:
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APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-991-867B-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION ATA:
APPLICATION NUMBER: WO 92/14818
FILING APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF-114.C3
TELLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 64.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-07-991-867B-43 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-485-529-104 x US-07-991-867B-43
                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic)
US-07-991-8678-43
INFORMATION FOR ESQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 235 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      3.727
78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32606
                                                                                                                                                                                                                                                                 Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Hall, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
WIMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-544-332-45
                                                                                                                                                                     Gaps: 0
Percent Identity: 64.286
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE:
                                                                                                                                                                                                                                                                                                                                 2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-544-332-43 from: 1 to: 235
                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-AM-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       us 08/107,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/107,75
FILING DATE: 19-AUG-1993
FILING PAPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
; Sequence 45, Application US/08544332
; Detent No. 5935777
; GENERAL INFORMATION:
                                                                                                                                                                                                                             alignment_block:
US-09-485-529-104 x US-08-544-332-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45:
                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-544-332-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bencen, Gerard H. REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 235 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                          41.00
3.727
78.571
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single
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                                                                                                                                             Quality:
Ratio:
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STRANDEDNESS:
                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32606
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COUNTRY: U
                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
CORRESPONDENCES: 77
                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-544-332-43
                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 64.286
                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-07-991-867B-45 from: 1 to: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
                                                                                                                                                                                                                                                                                                                                   2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION 1935

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION NUMBER: US 07/857,584
FILING DATE: 19-FEB-1991
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UF114.C4
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US-09-485-529-104 x US-07-991-867B-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 35,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS:
                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-991-867B-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bencen, Gerard H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 235 base pairs
TYPE: nucleic acid
                                                                                                                                                                     3.727
78.571
                                                                                                                                               41.00
single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
STRANDEDNESS:
                                                                                                                                                                  Ratio:
Percent Similarity:
                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32606
                                                                                                                         alignment_scores:
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alignment_scores

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:q_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-424-224-1
                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 64.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 GAATTATTGAACGTCAAAGGTTATCCTGTTAAAGCATCCGAT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lign seg 1/1 to: US-08-544-332-45 from: 1 to: 235
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PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FFILER
REGISTRATION NUMBER: 26,28
REFERENCE/DOCKET NUMBER: 20.26-406
TELECOMONICATION INFORMATION:
'TELEPHONE: 212-758-4800
TELEFAX: 212-758-4800
TELEFAX: 212-758-4800
TELES: 421792
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARRACTERISTICS:
LENGTH: 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08424224
Patent No. 5912173
GENERAL INFORMATION:
TITLE OF INVENTION: MURINE IL-2R
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ignment_block:
S-091485-529-104 x US-08-544-332-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESCRIPTION: OLIGONUCLEOTIDE
                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
08-544-332-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: MURINE
; INDIVIDUAL ISOLATE: IL-2R
US-08-424-224-1
                                                                                                                                                                                                                                                                                                                                                                     3.727
78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
    single
                                                                                                                                                                                                                                                                                                                 41.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                          srcent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: UN
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                           ignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NI
COUNTRY:
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seq_documentation_block:
    Sequence 68, Application PC/TUS9402891
    GENERAL INFORMATION:
    APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
    APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
    APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
    APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA
    TITLE OF INVENTION: XSCID
    NUMBER OF SEQUENCES: 69
                                                                                                                                                   to: 1608
                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-02891-68
Length: 13
Gaps: 0
Percent Identity: 69.231
                                                                                                                                                 Align seg 1/1 to reverse of: US-08-424-224-1 from: 1
                                                                                                                                                                                          SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2026-4061
                                                                                   alignment_block:
US-09-485-529-104 x US-08-424-224-1/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,143
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY_AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-406
TELEPHONE: 212-758-4800
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
CMEDUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; INDIVIDUAL ISOLATE: IL-2R
PCT-US94-02891-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608
41.00
3.727
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                        Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
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alignment_scores

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alignment_scores
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Sequence 12, Application US/09090793

Patent No. 6140486

GENERAL INFORMATION:

APPLICANT: Calgene, LLC

TITLE OF INVENTION: Production of polyunsaturated fatty acids by expression

TITLE OF INVENTION: Of polyketide-like synthesis genes in plants

TITLE OF INVENTION: Of polyketide-like synthesis genes in plants

TITLE OF INVENTION: 01 polyketide-like synthesis genes in plants

CURRENT APPLICATION NUMBER: US/09/090,793

CURRENT FILING DATE: 1998-06-04

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 12

LENGTH: 40138
                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
    Sequence 13, Application US/09090793
    Patent No. 6140486
    GENERAL INFORMATION:
    TITLE OF INVENTION: Production of polyunsaturated fatty acids by expr.
    TITLE OF INVENTION: Production of polyunsaturated fatty acids by expr.
    TITLE OF INVENTION: Production of polyunsaturated fatty acids by expr.
    TITLE OF INVENTION: De POLYKetide-like synthesis genes in plants
    FILE REFERENCE: CGNE.13: 0100S
    CURRENT FILING DATE: 1998-06-04
    EARLIER FILING DATE: 1997-06-04
    NUMBER OF SEQ ID NOS: 66
    SOFTWARE: PatentIn Ver. 2.0
    SEQ ID NO 13
    LENGTH: 19227
                                                                                                                                                                                     Align seg 1/1 to reverse of: PCT-US94-02891-68 from: 1 to: 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: US-09-090-793-13 from: 1 to: 19227
                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-090-793-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-090-793-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0
Percent Identity: 80.000
                                Gaps: 0
Percent Identity: 69.231
                                                                                                                                                                                                                                   13732 GAACTGATACTTGCGCTTGGGTATAAAGTC 13703
                                                                                                                               US-09-485-529-104 x PCT-US94-02891-68/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GluLeuLeuAlaAlaLeuGlyTyrLysVal 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-485-529-104 x US-09-090-793-13/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.00
4.444
90.000
41.00
3.727
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Vibrio marinus
US-09-090-793-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Vibrio marinus US-09-090-793-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seg_documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Manmias, Clara
APPLICANT: Benorine, Jean L.
APPLICANT: Strosbergio Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691155th Carolina
COUNTRY: USA
                                                                                                                                          to: 40138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 298
                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-087-772A-7
                                                                                                                                          Align seg 1/1 to reverse of: US-09-090-793-12 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: US-08-087-772A-7 from: 1
                        Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/087,772A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GluLeuLeuAlaAlaLeuGlyTyrLysVal 11
                                                                                alignment_block:
US-09-485-529-104 x US-09-090-793-12/rev
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US-09-485-529-104 x US-08-087-772A-7/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3339-195
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3335:
TELECOMMUNICATION INFORMATION:
TELEFAX: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-08-087-772A-7
40.00
4.444
90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 298 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.00
3.545
84.615
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                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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Quality:
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      Quality:
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Sequence 4, Application US/08087772A
Sequence 4, Application US/08087772A
Patent No. 5691155
GENERAL INFORMATION:
APPLICANT: Nahmias, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
              GENERAL INFORMATION:
APPLICANT: Nahmias, Clara
APPLICANT: Nahmias, Clara
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-087-772A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 13
Gaps: 0
Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: US-08-087-772A-3 from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
                                                                                                                                                                                                       ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-485-529-104 x US-08-087-772A-3/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3339-195
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CITY: Charlotte
STATE: No. 5691155th Carolina
                                                                                                                                                                                                                     STREET: Post CITY: Charlotte
STATE: No. 5691155th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 33399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-087-772A-3
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-087-772A-3
g_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-276-531-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
GORRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 703
                                                                                                                                                                                                                                                                                                                                                                                           E: INCYTE PHARMACEUTICALS, INC 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: US-09-276-531-31 from: 1
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Sequence 3, Application US/08087772A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
CLASSIFICATION:
                                                                Sequence 31, Application US/09276531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATORNEY AGENT INFORMATION:
NAME: Lynn E. Murry, Ph.D.
REGISTATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0C
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFRAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .ignment_block:
is-09-485-529-104 x US-09-276-531-31
                                                                                                         GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
                                                                                                                                                                                                                        APPLICANT: Reddy, Roopa
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 703 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 3.900 ercent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: | MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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                                                _documentation_block
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lign seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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TELECOMMUNICATION INFORMATION: TELEPHONE: 919-881-3140
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TELEFAX: (202) 789-1158
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                               CDS
568..1731
                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-08-087-772A-1
                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nahmias, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Extrosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-087-772A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lign seg 1/1 to reverse of: US-08-087-772A-4 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 69.231
                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Bell, Seltzer, Park & Glbson STREET: Post Office Drawer 34009 CITY: Charlotte STATE: No. 5691155th Carolina COUNTRY: USA
                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 800
ATTONNEY/AGENT INFORMATION:
NAME: LINKET, RAYMOND 0.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECHOME: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ignment_block:
S-09-485-529-104 x US-08-087-772A-4/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q_documentation_block:
Sequence 1, Application US/08087772A
Patent No. 5691155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1360 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,4
REFERENCE/DOCKET NUMBER:
                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.545
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |gnment_scores
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to: 1920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
    Sequence 3 Application Us/08450962
    Patent No. 6274706
    Patent No. 6274706
    Sequence 3. Application Us/08450962
    Patent No. 6274706
    APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
    TITLE OF INVENTION: GENES
    NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS: ADDRESSE: RECK, MAHIN & CATE
    STREET: P.O. BOX 06110
    CITY: CHICAGO
    STATE: ILLINOIS
    COMPREY: US.A.
    COMPUTER READABLE FORM:
    MEDIUM TYPE: 3.1/2 diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: US-08-087-772A-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,829
FILING DATE: 08-SEPT-1993
APPLICATION NUMBER: 07/721,571
FILING DATE: 25-MAY-1990
PRIOR APPLICATION NUMBER: PCT/FR89/00918
FILING DATE: 25-JAN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleit, Martin; Gollin, Michael REGISTRATION NUMBER: 16,900; 31,957
REFERENCE/DOCKET NUMBER: 47078-042
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-485-529-104 x US-08-087-772A-1/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,962
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: 3-1/2" diskette IBM compatible
                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: ASCII
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 1920 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 39.00
Ratio: 3.545
Percent Similarity: 84.615
                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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to: 1491

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1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16
                                          Align seg 1/1 to: US-08-137-614A-3 from: 1
US-09-485-529-104 x US-08-137-614A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Knipple, Douglas C.
APPLICANT: Henderson, Joseph E.
TITLE OF INVENTION: Gene Encoding An Insect
TITLE OF INVENTION: Gamma-Aminobutyric Acid (GABA) Receptor Subunit
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          to: 3437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-137-614A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: THE PC COMPAGE SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/137,614A

FILING DATE: 15-OCT-1993

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                          lign seg 1/1 to reverse of: US-08-450-962-3 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0
Percent Identity: 43.750
                                                                                                                                                                                                                                    Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                        3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/POCKET NUMBER: 19603/120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1636
TELEFAX: (716)263-1600
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                            ignment_block:
S-09-485-529-104 x US-08-450-962-3/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q_documentation_block:
Sequence 3, Application US/08137614A
Patent No. 5487976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
      ENGTH: 343/ DECT TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.455
                                                                                                                                                                                     39.00
3.545
84.615
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                               ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                int_scores:
                                                                                  TOPOLOGY:
                                                                                                                                                                        gnment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16
                                              seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-768-301-1
                                                                                                                                                                                                                ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond STREET: 30 Rockefeller Plaza CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 43.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-768-301-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A30693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: MacLeod, Janet M
REGISTRATION UNMBER: 35,263
REFERENCE/DOCKET NUMBER: A306
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-485-529-104 x US-08-768-301-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.455
68.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                            RY: U.S.A.
10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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12936..13487

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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAGES:
                                                                                                                                                                                         FEATURE:
                                                                seq_documentation_block:
    Sequence 14, Application US/08799464A
    Sequence 14, Application US/08799464A
    Patent No. 2998601
    GENERAL INFORMATION:
    APPLICANT: Murtaugh, Michael P. et al.
    TITLE OF INVENTION: WETHODS OF USE
    TITLE OF INVENTION: METHODS OF USE
    NUMBER OF SEQUENCES: 35
    CORRESPONDENCE ADDRESS:
                        seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-799-464A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/799,464A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 212.7402
LOCATION: 212.77402
OTHER INFORMATION: /citation= "LV ORF 1a"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
'LOCATION: 12394..13191
OTHER INFORMATION: /standard_name= "LV ORF 3"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
!LOCATION: 11796..12535
UPTER INFORMATION: /standard_name= "LV ORF 2"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OD: experimental /evidence= EXPERIMENTAL
                                                                                                                                                                                                                                                                                  ADDRESSEE: John M. Collins
STREET: 2405 Grand Blvd., Suite 400
CITY: Kansas City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= ORF1b
/citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/287,941
FILING DATE: August 5, 1994
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 22907
TELEPHONE: (816) 474-9050
TELEPHONE: (816) 474-9057
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15101 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | NAME/KEY: misc_feature
| LOCATION: 7384..11775
| IDENTIFICATION METHOD: e
| OTHER INFORMATION: /evid
| OTHER INFORMATION: /labe
| OTHER INFORMATION: /labe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Arteriviridae
STRAIN: VR-2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                          STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US95-09927-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9088 GACCGCATCCTGGCTGCTTGCATATCACATGAAGGCGCAGAAC 9132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; RELEVANT RESIDUES IN SEQ ID NO: 14: FROM 1 TO 15101
US-08-799-464A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moormann, R. J.
Lelystad virus, the causative agent of
procine epidemic abnortion and respiratory
syndrome (PEARS) is related to LDV and EAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.25
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OTHER INFORMATION: /citation= ([1])
OTHER INFORMATION: /standard_name= "LV ORF 4" OTHER INFORMATION: /citation= ([1])
                                                                                             "LV ORF 5"
                                                                                                                                                                                                                                                                                       "LV ORF 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-799-464A-14 from: 1
                                                                         LOCATION: 13484.14089
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OTHER INFORMATION: /citation- ([1])
PUBLICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0 v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: John M. Collins
STREET: 1101 Walnut, Suite 1400
CITY: Kansas City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-485-529-104 x US-08-799-464A-14
                                                                                                                                                                                                                                                                                                                                                   Meulenberg, J. J.M
                                                                                                                                                                                                                                                                                                                                                                   Hulst, M. M.
de Veijer, E. J.
Moonen, P. L.
den Besten, A.
de Kluyver, E. P.
Wensvoort, G.
                                                         NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.714
93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Kansas Cit
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE: SY
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS:
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AUTHORS:

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NAME/KEY: misc_feature
LOCATION: 212.7402
LOCATION: 2/2.7402
LOCATION: 2/2.7402
OTHER INFORMATION: /citation= ([1])
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NAME/KEY: misc_feature
LCCATION: 11786..125355
OTHER INFORMATION: /standard_name= "LV ORF 2"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 14588..14974
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OTHER INFORMATION: /citation= ([1])
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LOCATION: 12394..13191
OTHER INFORMATION: /standard_name= "LV ORF 3"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 12936.1346.13467
Atandard_name= "LV ORF 4"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANUME:
NAME/KEX: misc_feature
LOCATION: 7384..11775
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /label= ORFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 14077.14598
OCHER INFORMATION: /citation= "LV ORF
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 13484.14089
OTHER INFORMATION: /citation= "LV ORF
OTHER INFORMATION: /citation= ([1])
              APPLICATION NUMBER: PCT/US95/09927
FILING DATE:
CLASSIPLATION:
RATIONREY/SERVI INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 2297
REFERENCE/DOCKET NUMBER: 2297
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEPHONE: (816) 474-9057
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGHH: 1510 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
RATII-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arteriviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meulenberg, J. J.M.
Hulst, M. M.
de Veijer, E. J.
Moonen, P. L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        den Besten, A.
de Kluyver, E. P.
Wensvoort, G.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS:
AUTHORS:
AUTHORS:
AUTHORS:
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Seguence 1, Application US/08157005
; Sequence 1, Application US/08157005
; Patent No. 5620691
; GENERAL INFORMATION:
    APPLICANT: Wensvoort, Gert
    APPLICANT: Wensvoort, Gert
    APPLICANT: Medlenbertus J
    APPLICANT: Medlenbertus J
    APPLICANT: Medlenberty Johannes M
    APPLICANT: Medle
                                                           TITLE: Lelystad virus, the causative agent of TITLE: procline epidemic abnortion and respiratory TITLE: syndrome (PEARS) is related to LDV and EAV. VOLUME: 192 PAGES: 62-72 PAGES: 62-72 PAGES: 62-72 PAGES: 193 PATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-157-005-1
. Moormann, R. J. Lelystad virus, the causative agent of procine epidemic abnortion and respiratory syndrome (PEARS) is related to LDV and EAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: PCT-US95-09927-14 from: 1 to: 15101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTUR RELEASE #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,005
FILING DATE: 26-NOV-1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92200781.0
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92200781.0
FILING DATE: 05-JUN-1992
ATTORNEY/AGENT INFORMATION:
REJESTRATION NUMBER: 16,579
REFERENCE/DOCKET NUMBER: 44819
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-485-529-104 x PCT-US95-09927-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.714 93.333
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10112
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FILING DATE:
CLASSIFICATION:
PRICK APPLICATION DATA:
PRICK APPLICATION DATA:
APPLICATION NUMBER:
ILING DATE: 26-NOV-1993
PRICK APPLICATION DATA:
APPLICATION NUMBER: EP 91201398.4
FILING DATE: 06-JUN-1991
PRICK APPLICATION DATA:
APPLICATION NUMBER: EP 92200781.0
FILING DATE: 18-MAR.1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: EP 92200781.0
FILING DATE: 05-JUN-1992
ATTORNEY,AGENT INFORMATION:
NAME: TUNNEY, Alben C.
REGISTRATION NUMBER: 33041
REFERRUCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (801) 531-9168
INFORMATION FOR SEQ ID NO: 1:
TELEFAX: (801) 532-1922
ILENGTH: 15108 base pairs
ILENGTH: 15108 base pairs
TYPE: nucleic acid
STRANDEDSES: single
                                                                                                                                                            SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,863
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 212..7399
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: 7384..11772
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 11786..12532
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 12394..13188
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 13484..14086
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 12936..13484
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14077..14595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 14077...
OTHER INFORMATION:
                          Utah
  CITY: Sal
STATE: Ut
COUNTRY:
ZIP: 8411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pa_documentation_block:
Sequence 1, Application US/08747863
Fatent No. 6197310
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wensvoort, Gert
APPLICANT: Terpstra, Catharinus
APPLICANT: Pol, Johannes
APPLICANT: Meulenberg, Johanna J
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-747-863-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.00 Length: 15
2.714 Gaps: 0
93.333 Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lign seg 1/1 to: US-08-157-005-1 from: 1 to: 15108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Trask, Britt & Rossa
STREET: 525 South 300 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1gnment_block:
S-09-485-529-104 x US-08-157-005-1
                                                                                                                       MOLECULE TYPE: DNA (genomic)
FEATURE:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 11786..12532
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 14077..14595
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 12394..13188
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 13484..14086
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 14588..14971
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 12936..13484
OTHER INFORMATION:
                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 7384..11772
OTHER INFORMATION:
                                                                                                                                                            NAME/KEY: CDS
LOCATION: 212..7399
OTHER INFORMATION:
                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lignment_scores:
Quality:
`Ratio: ?
Percent Similarity:
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us-09-485-529-104.p2n.rni

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GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS AND GRAHAM F. HATFULL
TITLE OF INVENTION: D29 SHUTTLE PHASMIDS AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-614-770A-1
                                                                                                                                                                                                                                           1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     percent Identity: 66.667
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                                                                                                                                                                        Align seg 1/1 to: US-08-747-863-1 from: 1 to: 15108
                                                               Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/614,770A
FILING DATE: MARCH 7, 1996
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERNEX/POCKET NUMBER: 96700/402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
; Sequence 1, Application US/08614770A
; Patent No. 5773267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-485-529-104 x US-08-614-770A-1
                                                                                                         alignment_block:
US-09-485-529-104 x US-08-747-863-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION: OLIGONUCLEOTIDE POTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: MYCOBACTERIOPHAGE;
INDIVIDUAL ISOLATE: D29
US-08-614-770a-1
                  38.00
2.714
93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUDENCE 492/2
LENGTH: 492/2
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: NEW YORK COUNTRY: U.S.A. ZIP: 10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEW YORK
                      Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Mohr, Christine
APPLICANT: Knechtle, Philipp
APPLICANT: Knechtle, Philipp
APPLICANT: Resischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-998-416-955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0
Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: PATENTEN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                      seq_documentation_block:
Sequence 955, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-485-529-104 x US-08-998-416-955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-998-416-955
                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.364
73.333
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAG1590RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 24
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
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Sequence 1015, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.364
73.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                     ZIP: 27709
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US-08-998-416-189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Resischung, Corinn
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 642
q_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-998-416-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-998-416-189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 CIGCIAAAACIACICGGGIAICGAAICCGAIIIGCIACIIIAGCC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lign seg 1/1 to reverse of: US-08-998-416-192 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
CUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FALENCE.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION 1435
PRIOR APPLICATION OF 135
ATORNEYAGENT INFORMATION:
NAME: Me19s, J. Timothy
REGISTRATION NUMBER: 38,241
REFRENCE/POCKET NUMBER: PF/5-303(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 192:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 base pairs
TYPE: NUCLEIC acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ignment_block:
S-09-485-529-104 x US-08-998-416-192/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g_documentation_block:
Sequence 189, Application US/08998416
Patent No. 6239264
                                        q_documentation_block:
Sequence 192, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NO. COUNTRY: US ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-998-416-192
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APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Wond, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rebisching, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS: 1
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR DATE: 31-DEC-1996
FILING DATE: 31-DEC-1996
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Melgs, J. Timothy
REGISTRATION NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMUNICATION:
TELECOMMUNICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: No. 6239264artis Corporation STREET: 304 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-485-529-104 x US-08-998-416-189/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
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Rebischung, Corinne
/ENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                     DNA SEQUENCES OF ASHBYA GOSSYPII
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                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy DISK
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: CT 0016/97
FILING DATE: 31-DEC-1996
ATTONEX/AGENT INFORMATION:
ANALYMENTAGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
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                                                                                                                                                                 No. 6239264artis Corporation
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TITLE OF INVENTION: GENOMIC DNA SEQUI
TITLE OF INVENTION: AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: GENOMIC DNA SEQU
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
    Sequence 386, Application US/08998416
    Patent No. 6239264
    Factor No. 6239264
    Sequence 3862624
    APPLICANT: Philippsen, Peter
                                                                                                                                                                                     STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1015:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
Wendland, Jurgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio: 3.364
Percent Similarity: 73.333
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MOLECULE TYPE: D
ORIGINAL SOURCE:
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Quality:
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                                                                                                                                                                 ADDRESSEE:
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APPLICANT:
APPLICANT:
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APPLICANT:
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to: 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 CIGCIAAAACTACICGGGIAICGAAICCGAITIGCIACITIAGCC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: US-08-998-416-386 from: 1
                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION TAN
APPLICATION NUMBER: US/08/998,416
ATFORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
FILECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 919-541-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0

Percent Identity: 46.667
STREE: No. 6239264artis Corporation STREE: No. 6239264artis Corporation CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; No. 6239264artis Corporation 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Philippsen, Peter
APPLICANT: Pollmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUEN
MINDER OF INVENTION: APD USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-485-529-104 x US-08-998-416-386/rev
                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 798 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 62392
STREET: 3054 Cornwal
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM:
US-08-998-416-386
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19911217

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Sequence 14, Application US/07809457A
Patent No. 5512466
GENERAL INFORMATION:
APPLICANT: Klee, Harry J.
APPLICANT: Klee, Tarry J.
TITLE OF INVENTION: Control of Fruit Ribening and Senescence TITLE OF INVENTION: 1n Plants
NUMBER OF SEQUENCES: 17
CORRESPONDERES: 17
APPLICANT: CARRESPONDERES: 17
APPLICANT: CARRESPONDERES: 17
APPLICANT: CARRESPONDERES: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 CTGCTAAAACTACTCGGGTATCGAATCCGATTTGCTACTTTAGCC 406
                                                                                                                                                                                OURTHAIN SISTEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CF 0016/97
FILING DATE: 31-DEC-196
ATTORNEY/AGENT INFORMATION:
NAME: Me198, J. TIMOCHY
REGISTRATION NUMBER: 38,241
REFERENCE/CDCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1997
TELECOMMUNICATION 1997
TELECOMMUNICATION 1997
TELECOMMUNICATION 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-998-416-497 from: 1 to: 832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/809,457A
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-485-529-104 x US-08-998-416-497
No. 6239264th Carolina
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 497:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.364
73.333
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM:
US-08-998-416-497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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APPLICANT: Barry, Gerard F.
APPLICANT: Barry, Granesh M.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-476-008-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-07-809-457A-14 from: 1 to: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                            NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REGISTRATION NUMBER: 30,914
REERENENCAPOCKET NUMBER: 38-21(10538)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-609
INFORMATION.FOR SEQ ID NO: 14:
SEGUENCE CHARACTERISTICS:
LENGTH: 1377 base pairs
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: HOEFINE JF., Dennis R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-485-529-104 x US-07-809-457A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
; Sequence 9, Application US/08476008
; Patent No. 5627061
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.00
3.083
85.714
                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                            TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           St. Louis
Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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STATE:
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38-21(10660)A

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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63198
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                                                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08306063
Sequence 9, Application US/08306063
Sequence 9, Application US/08306063
Settent No. 5633435
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Rishore, Ganesh M.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seg_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-306-063-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-476-008-9 from: 1 to: 1377
                                                                                                               38-21(10660)A
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
           CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: HOEINET JT., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOOKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1377 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-485-529-104 x US-08-476-008-9
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                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-476-008-9
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FILING DATE: 31-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 3.083
Percent Similarity: 85.714
                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 700 Ches
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
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seq_documentation_block:

Sequence 14, Application US/08553943

Patent No. 570233

GENERAL INFORMATION:

APPLICANT: Klee, Harry J.

APPLICANT: Kishore, Ganesh M.

TITLE OF INVENTION: Control of Fruit Ripening and Senescence;

TITLE OF INVENTION: in Plants

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-553-943-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,943
FILING DATE: 06-NOV-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/809,457
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: HOETNEY JF., Dennis R.
REGISTRATION NUMBER: 30,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 14 Gaps: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-306-063-9 from: 1 to: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10538)A
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-485-529-104 x US-08-306-063-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEPAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1377 base pairs
                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
WOLECULE TYPE: DNA (genomic)
US-08-306-063-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (314)537-6099
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US-08-833-485-9
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APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-833-485-9
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COFTANTION STSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-ANG-1991
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-ANG-1990
CLASSIFICATION: A35
PRIOR APPLICATION: A35
PRIOR APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1314 GATTTGATGGCTGGTCTTGGAGCTAAGATCGAACTCTCCGAC 1355
                                                                                                                                                                                                                                                                                                                                        Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REPERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-485-529-104 x US-08-553-943-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
    Sequence 9, Application US/08833485
    Patent No. 5804425
; MOLECULE TYPE: DNA (genomic)
US-08-553-943-14
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (314)737-6099
TELEFAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                          Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
TUTHER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Dennis R. Hoerner, Jr., Monsanto Co. BB4F 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-137-440-9
                                                                                                                                                                                                                                                                                      Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,440
                                                                                                                                                                                                                                                            2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                      Align seg 1/1 to: US-08-833-485-9 from: 1 to: 1377
                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38-21(15117)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US 08/33,485
FILING DATE: 07-APR-1997
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
PRIOR APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION NUMBER: US 07/56,537
APPLICATION NUMBER: US 07/576,537
ATTORNEY APPLICATION NUMBER: US 07/576,537
ATTORNEY APPLICATION NUMBER: US 07/576,537
ATTORNEY ARENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
; Sequence 9, Application US/09137440
; Sequence 9, Each No. 6248876
; GENERAL INFORMATION:
                                                                                                                              alignment_block:
US-09-485-529-104 x US-08-833-485-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: HOERDER Jr., Dennis R. REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) US-09-137-440-9
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INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 1377 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (314)737-6099
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STRANDEDNESS: double
TOPOLOGY: linear
                                             Ratio: 3.083
Percent Similarity: 85.714
                          37.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
alignment_scores:
Quality:
Ratio:
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Align seg 1/1 to: PCT-US91-06148A-9 from: 1 to: 1377
                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
    Sequence 9, Application PC/TUS9106148A
    Sequence 9, Application PC/TUS9106148A
    Sequence 9, Application PC/TUS9106148A
    Septicant: Barry, Gerard F.
    APPLICANT: Rishore, Ganesh M.
    APPLICANT: Padgette, Stephen R.
    TITLE OF INVENTION: Glyphosate Tolerant
    TITLE OF INVENTION: Glyphosate Tolerant
    TITLE OF SEQUENCES: 36
    NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US91-06148A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE PATENTIN STILLS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06148A
FILING DATE: 19910828
CLASSIFICATION BOO
PRIOR APPLICATION TAA:
APPLICATION NUMBER: US/07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 50.000
                                                                                                                                                                                                                                                              2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                               Align seg 1/1 to: US-09-137-440-9 from: 1 to: 1377
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TELECOMMUNICATION INFORMATION:
TELEBRAX: (314)537-6099
TELEBRAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-485-529-104 x PCT-US91-06148A-9
                                                                                                                                         alignment_block:
US-09-485-529-104 x US-09-137-440-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: HOErner Jr., Dennis R. REGISTRATION NUMBER: 30,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1377 base pairs
TYPE: NUCLEIC ACID
                                            37.00
3.083
85.714
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3.083
85.714
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STATE: Missouri
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                                                                   Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                 Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63198
                      alignment_scores
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Fruit Ripening and Senescence
                                                                                   seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US91-09437-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: PCT-US91-09437-14 from: 1 to: 1377
                                         1314 GATTTGATGGCTGGTCTTGGAGCTAAGATCGAACTCTCCGAC 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 14
Gaps: 0
Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: PCT/US91/09437
FILING DATE: 19911217
2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                     700 Chesterfield Village Parkway
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19911217
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 Sequence 14, Application PC/TUS9109437 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-485-529-104 x PCT-US91-09437-14
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APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: CONTCOl of
TITLE OF INVENTION: in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hoerner Jr., Dennis R. REGISTRATION NUMBER: 30,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
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APPLICANT: Barry, Gerard F.
                                                                                                                                                                                                                                                                                                                                     Monsanto Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                  STREET: 700 Chesciff: St. Louis
STATE: Missouri
COUNTRY: USA
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                                                                                                                              seq_documentation_block
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 63198
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APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                       ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-306-063-2
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-406-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/76,537
FILING DATE: 31-406-1991
CLASSIFICATION NUMBER: US 07/576,537
ATTONIEY/AGENT INFORMATION:
ATTONIEY/AGENT INFORMATION:
NAME: NOATHORY INFORMATION:
NAME: NOATHORY INFORMATION:
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Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: HOERNE Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REPERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block: .
US-09-485-529-104 x US-08-476-008-2
Kishore, Ganesh M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1982 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Barry, Gerard F.
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62..1426
                                                                                                                                                                             STREET: 700 Chest CITY: St. Louis STATE: Missouri
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                    USA
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US-08-476-008-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-833-485-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE STATES OF THE STATES 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
    Sequence 2, Application US/08833485
    Patent No. 5804425
    GENERAL INFORMATION:
    APPLICANT: Barry, Gerard F.
    APPLICANT: Rahore, Ganesh M.
    APPLICANT: Padgette, Stephen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-485-529-104 x US-08-306-063-2
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NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
Kishore, Ganesh M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 3
TELECOMMUNICATION INFORMATION
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TELEFRAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2
SEQUIENCE CHARACTERISTICS:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63198
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COCATION:
US-08-306-063-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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APPLICANT: Barry, Gerard F.
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                       STREET: 700 Chest CITY: St. Louis STATE: Missouri COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         63198
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; LOCATION:
US-09-137-440-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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                               TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F STREET: 700 Chesterfield Village Parkway CITY: St. Louis STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-137-440-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OURTHAING SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
TLING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
CLASSIFICATION NUMBER:
BRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
CLASSIFICATION:
APPLICATION NUMBER:
BRIOR APPLICATION:
APPLICATION NUMBER:
CLASSIFICATION:
APPLICATION NUMBER:
BRIOR APPLICATION A35
PRIOR APPLICATION NUMBER:
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
APPLICAT
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Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
; Sequence 2, Application US/09137440
; Patent No. 6248876
; GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
Stallings, William C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-485-529-104 x US-08-833-485-2
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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85.714
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                       ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.00
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; LOCATION: 62..
US-08-833-485-2
                                                                                                                                                                                                                                                                                                                                               USA
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APPLICANT:
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APPLICANT: Redgette, Stephen R.
APPLICANT: Railings (1) Hillan C.
TITLE OF INVERTION: Glyphosate Tolerant
MUMBERS OF SEQUENCES:
MUMBERS OF SEGUENCES:
MUMB
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APPLICANT: KUMABARA, YOKO

APPLICANT: RAMATSU, TSUYOSHI
APPLICANT: NAKAMATSU, TSUYOSHI
APPLICANT: NORAHASHI, Osamu
APPLICANT: NORAHASHI, Osamu
APPLICANT: TO, HISAO
TITLE OF INVENTION: CARBAMOYL-PHOSPHATE SYNTHETASE GENE OF CORYNEFORM
TITLE OF INVENTION: BACTERIA AND METHOD FOR PRODUCING L-ARGININE
FILE REPERENCE: OP945CIP
CURRENT APPLICATION NUMBER: US/09/629,616
CURRENT APPLICATION NUMBER: 12000-07-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALEGELIN Ver. 2.0
SEQ ID NO 1
                STREET: Steuart Street Tower, 20th Floor, One Market STREET: Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-629-616-1
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/106,761
FILING DATE: 19930813
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 2307E-445
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9601
TELEPHONE: (415) 543-9603
TELEPHONE: CHARACTERISTICS:
LENGTH: 2101 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 61.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-106-761-1 from: 1 to: 2101
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    Sequence 1, Application US/09629616
    Patent No. 6255086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-485-529-104 x US-08-106-761-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.00
4.111
69.231
                                                       San Francisco
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Ratio:
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LOCATION:

US-08-106-761-1
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                                                       CITY: Sar
STATE: CA
                APPLICANT: Padgette, Stephen R.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: HAMMOCK, Bruce D.
APPLICANT: GRANT, David F.
APPLICANT: GETHAM, Jeffrey K.
TITLE OF INVENTION: RECOMBINANT SOLUBLE EPOXIDE HYDROLASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                    ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-106-761-1
                                                                                                                                                                                                                                    Align seg 1/1 to: PCT-US91-06148A-2 from: 1 to: 1982
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Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: HOETNET JT., Dennis R.
REGISTRATION NUMBER: 30,914
REPERENCE/DOCKET NUMBER: 38-21(10535)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-485-529-104 x PCT-US91-06148A-2
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    Sequence 1, Application US/08106761
    Patent No. 5445956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1982 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.00
3.083
85.714
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EDNESS: double
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Ratio:
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                                                                                                                                                                                                                            63198
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LOCATION:
PCT-US91-06148A-2
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APPLICANT:
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TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 27
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/182,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-182-117-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-182-117-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2258 GATTTGATGGCTGGTCTTGGAGCTAAGATCGAACTCTCCCGAC 2299
                                                                                                                                                                                                                                             Length: 12
Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 0
Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-629-616-1 from: 1 to: 4837
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Brevibacterium lactofermentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
    Sequence 5, Application US/09182117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
; Sequence 1, Application US/09182117
; Patent No. 620436
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-485-529-104 x US-09-182-117-1
                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-485-529-104 x US-09-629-616-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8012 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ANTI-SENSE: NO
US-09-182-117-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                          alignment_scores:
LENGTH: 4837
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TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/182,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-182-117-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
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Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-09-182-117-5 from: 1 to: 8418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/182,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eq_documentation_block:
Sequence 4, Application US/09182117
Patent No. 6204436
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-485-529-104 x US-09-182-117-5
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                              CLASSIFICATION:
INFORMATION FOR SEQ 1D NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8418 base palrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 8798 base pairs
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
Patent No. 6204436
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NATI-SENSE: NO
                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-182-117-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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join(4378..4443, 22026..22106, 23001..23483,
23905..24039, 24251..24418)
                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-472-217-1
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jaakkola, Panu
APPLICANT: Jaakkanen, Markku
APPLICANT: Lepp, Sirpa
APPLICANT: Wall, Markku
APPLICANT: Winnen, Tapani
APPLICANT: With Anni
TITLE OF INVENTION: Syndecan Stimulation Of Cellular
TITLE OF INVENTION: Differentiation
                                                                                                                                                                                             Percent Identity: 50.000
                                                                                                                                                                  2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                     to: 8798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sterne, Kessler, Goldstein & Fox
1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUGURERY PATENTIN Release #1.0, Version CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,217
FILING DATE: 07-JUN-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/206,186
FILING DATE: 07-MAR-1994
PRIOR APPLICATION NUMBER: US 07/988,427
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
AMME: Clinbala, Michale A.
REGISTRATION NUMBER: 33,851
REGISTRATION NUMBER: 33,851
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
CANDEL APPLICATION DATA:
CHENTH: CANDER AND SEC DE NO: 1:
SEQUENCE CHARACTERISTICS:
CHENTH: CANDER AND SEC DATES
                                                                                                                     Align seg 1/1 to: US-09-182-117-4 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Pal-
                                                                                                                                                                                                                                                                                                                            Sequence 1, App\overline{1}1cation US/08472217 Patent No. 5726058
                                               alignment_block:
US-09-485-529-104 x US-09-182-117-4
                                                                                                                                                                                                                                                                                                                                                                                                 Alanen-Kurki, Leena
Auvinen, Petri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JENGTH: 26700 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
Percent Similarity: 85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: LIVY
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Alanen-K
APPLICANT: Auvinen,
APPLICANT: Jaakkolla
APPLICANT: Jalkanen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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LOCATION:
US-08-472-217-1
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to: 26700
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jalkanen, Markku
APPLICANT: Jalkanen, Markku
APPLICANT: Mali, Markku
TITLE OF INVENTION: Suppression of Tumor Cell Growth By
TITLE OF INVENTION: Syndecan-1 Ectodomain
NUMBER OF SEQUENCES: 8
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., NW
                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-488-199-5
                                                                                                                                                                Align seg 1/1 to reverse of: US-08-472-217-1 from: 1
                                                       Percent Identity: 61.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSer 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOCTHWARE: FACENTIN RELEASE #1.0, VET
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,199
FILING DATE: 07-UN-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,862
FILING DATE: 13-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERNCE/DOCKET NUMBER: 1102.013000
TELEPHONE: 202-371-260
TELEPHONE: 202-371-260
TELEPHONE: 202-371-260
TELEPHONE: 202-371-260
TELEPHONE: CONTRACTERISTICS:
LENGHALION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGHI 26700 base pairs
                                                                                                    alignment_block:
US-09-485-529-104 x US-08-472-217-1/rev
                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
; Sequence 5, Application US/08488199
; Patent No. 5851993
; GENERAL INFORMATION:
              37.00
3.700
76.923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
24252..24418
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23002..23483
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23905..24040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDARD STREET: 1100 ...
CITY: Washington
                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: DC
COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
alignment_scores:
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FEATURE:
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; LOCATION:
US-08-488-199-5
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alignment_scores:
Quality: 37.00 Length: 13
Ratio: 3.700 Gaps: 0
Percent Similarity: 76.923 Percent Identity: 61.538
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alignment_block:
US-09-485-529-104 x US-08-488-199-5/rev ..
Align seg 1/1 to reverse of: US-08-488-199-5 from: 1 to: 26700